

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2005, 14:00:49 ; Search time 188 Seconds  
(without alignments)  
413.670 Million cell updates/sec

Title: US-10-706-801-1

Perfect score: 922

Sequence: 1 MFHVSFRYIFGLPPLVL.....RLIQIKTCWKILNGTEH 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A\_Geneseq\_21.\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	922	100.0	177	1 AAP1917	AAP1917 Derived s
2	922	100.0	177	2 AAR07627	AAR07627 Human int
3	922	100.0	177	2 AAR59919	AAR59919 Human int
4	922	100.0	177	2 AAR92796	AAR92796 Human int
5	922	100.0	177	2 AAW46467	AAW46467 Human int
6	922	100.0	177	2 AAY41595	AAY41595 Human int
7	922	100.0	177	2 AAB51092	AAB51092 Human int
8	922	100.0	177	6 ABP59504	ABP59504 Human int
9	922	100.0	177	7 ADD05356	ADD05356 Human int
10	922	100.0	177	7 ADC78857	ADC78857 Human PRO
11	922	100.0	177	7 ADI70851	ADI70851 Human int
12	922	100.0	177	7 ADN95217	ADN95217 Human BEC
13	922	100.0	177	8 ADM11079	ADM11079 Recombina
14	922	100.0	177	8 ADM11101	ADM11101 Human int
15	922	100.0	177	8 ADO50323	ADO50323 Human IL-
16	922	100.0	177	8 ADS87972	ADS87972 Tumour tr
17	922	100.0	177	9 ADY62267	ADY62267 Human int
18	922	100.0	177	9 ADY93810	ADY93810 Human int
19	922	100.0	177	9 ADZ26515	ADZ26515 Human IL7
20	922	100.0	177	9 AEB47779	AEB47779 Human int
21	922	100.0	345	9 ADY22158	ADY22158 Human IL-
22	919	99.7	177	9 ADY62268	ADY62268 Human int
23	917	99.5	177	9 ADY62270	ADY62270 Human int
24	917	99.5	177	9 ADY62269	ADY62269 Human int

25	916	99.3	177	9 ADY62271	ADY62271 Human int
26	895	97.1	177	8 ADM11088	ADM11088 IL-7 conf
27	895	97.1	177	8 ADM11102	ADM11102 Monkey in
28	815	88.4	173	8 ADM11094	ADM11094 IL-7 conf
29	814	88.3	159	6 ABR70789	ABR70789 Human ext
30	800.5	86.8	179	8 ADM11092	ADM11092 IL-7 conf
31	800	86.8	398	9 AEB47784	AEB47784 Mature hu
32	797	86.4	383	9 AEB47783	AEB47783 Mature hu
33	797	86.4	384	9 AEB47782	AEB47782 Mature hu
34	796	86.3	153	8 ADM11077	ADM11077 Recombina
35	796	86.3	391	9 AEB47786	AEB47786 Mature hu
36	796	86.3	393	9 AEB47785	AEB47785 Mature hu
37	788	85.5	173	8 ADM11098	ADM11098 IL-7 conf
38	775	84.1	157	8 AEB4582	AEB4582 Human dia
39	773.5	83.9	179	8 ADM11096	ADM11096 IL-7 conf
40	717	77.8	157	9 ADY25039	ADY25039 IL7-T8 sp
41	715	77.5	167	9 ADY25035	ADY25035 IL7-T7 sp
42	679.5	73.7	176	7 ADD05354	ADD05354 Sheep int
43	679.5	73.7	176	8 ADO50321	ADO50321 Sheep IL-
44	679.5	73.7	176	8 AEB47781	AEB47781 Sheep int
45	677.5	73.5	176	7 ADD05355	ADD05355 Cow inter

## ALIGNMENTS

RESULT 1	
AAP1917	
ID AAP1917	standard; protein; 177 AA.
XX	
AC AAP1917;	
XX	
DT 25-MAR-2003	(revised)
DT 14-MAY-1990	(first entry)
XX	
DE Derived sequence from a cDNA clone encoding human interleukin-7 (hIL-7).	
XX	
KW Human interleukin-7; hIL-7; lymphopoietic response;	
XX	
KW hematopoietic response; human liver adenocarcinoma cell line SK-HEP-1.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT Peptide	1..75
FT FT	/note="putative hydrophobic signal peptide"
FT Protein	76..177
XX	
PN EP314415-A.	
XX	
PD 03-MAY-1989.	
XX	
PF 24-OCT-1988;	88EP-00309977.
XX	
PR 26-OCT-1987;	87US-00113566.
XX	
PA (IMMV ) IMMUNEX CORP.	
XX	
PI Namen AE, Goodwin RG, Lupton SD, Mochizuki DY, Price VL;	
PI Deeley MC;	
XX	
DR WPI; 1989-131937/18.	
XX	
DR N-PSDB; AAN90783.	
XX	
PT Mammalian interleukin-7, analogues and sub-units - used for modulating or	
PT augmenting immune, lymphopoietic and/or haematopoietic response in	
PT mammals.	
XX	
PS Disclosure; Fig 5; 32pp; English.	
XX	
CC hIL-7 cDNA was isolated by cross-hybridisation studies using a probe	
CC derived from the hIL-7 cDNA (AAN90781) to screen human genomic DNA and	
CC cDNA libraries derived from cultures of the human liver adenocarcinoma	
CC cell line SK-HEP-1 (ATCC HTB-52). A plasmid bearing the coding sequence	



Query Match 100.0%; Score 922; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.6e-91;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60  
DB 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60

QY 61 NNEFNFKKHICDANKGMLFPAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFNFKKHICDANKGMLFPAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGQ 120

QY 121 VGRKPAALGEAQPYSLEENKSLKEOKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VGRKPAALGEAQPYSLEENKSLKEOKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177

RESULT 4  
AAR92796  
ID AAR92796 standard; protein; 177 AA.  
XX  
AC AAR92796;  
XX  
DT 24-MAY-1996 (first entry)  
XX  
DE Human interleukin-7.  
XX  
DE Cytokine; muten; interleukin-7; IL-7; agonist; antagonist; diagnosis;  
XX therapy; cancer; inflammation; degenerative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9604306-A2.  
XX  
PD 15-FEB-1996.  
XX  
PF 31-JUL-1995; 95WO-US008950.  
XX  
PR 01-AUG-1994; 94US-00284393.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Zurawski SM, Zurawski G;  
XX  
DR MPI; 1996-129335/13.  
XX  
PT Muten(s) of human and murine cytokine(s), esp. interleukin(s) and murine  
XX treatment of cancer, inflammation, etc.  
XX  
PS Disclosure; Page 38; 52pp; English.  
XX  
CC Mutens of human interleukin-7 (IL-7) (AAR92796) and other cytokines (see  
XX also AAR92790-95 and AAR92797-802) are obtd. by site-directed mutagenesis  
XX of natural cytokine sequences at positions identified as critical for  
XX activity. In IL-7, an amino acid substitution is made between helix B and  
XX helix C, and/or in helix D, giving mutens with partial agonist activity.  
XX The mutens are useful in the screening of cytokine and cytokine receptor  
XX levels, and in the diagnosis or treatment of e.g. inflammation, cancer,  
XX and degenerative disorders  
XX  
SQ Sequence 177 AA;

Query Match 100.0%; Score 922; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.6e-91;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60  
DB 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60

QY 61 NNEFNFKKHICDANKGMLFPAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGQ 120

DB 61 NNEFNFKKHICDANKGMLFPAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGQ 120  
QY 121 VGRKPAALGEAQPYSLEENKSLKEOKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VGRKPAALGEAQPYSLEENKSLKEOKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177

RESULT 5  
AAM46467  
ID AAM46467 standard; protein; 177 AA.  
XX  
AC AAM46467;  
XX  
DT 15-MAY-1998 (first entry)  
XX  
DE Human interleukin-7 (lymphopoietin-1).  
XX  
XX Interleukin-7; IL-7; lymphopoietin-1; LP-1; pre-B cell growth factor;  
XX development; proliferation; hematopoietic precursor; T cell; B cell;  
XX immunoreactive; antibody; detection; neutralisation; lymphokine.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
XX  
FT Peptide 1..26  
FT /note="signal peptide"  
FT Protein 27..152  
FT /note="mature protein"  
XX  
PN US5714585-A.  
XX  
PD 03-FEB-1998.  
XX  
PF 21-APR-1994; 94US-00231205.  
XX  
PR 26-OCT-1987; 87US-00113566.  
XX  
PR 07-OCT-1988; 88US-00255209.  
XX  
PR 13-APR-1990; 90US-00511438.  
XX  
PR 06-OCT-1992; 92US-00957649.  
XX  
PA (STER ) STERLING WINTHROP INC.  
XX  
PI Lupron SD, Mochizuki DY, Goodwin RG, Namen AB;  
XX  
DR MPI; 1998-129912/12.  
XX  
DR N-PSDB; AAV05147.  
XX  
PT New antibodies reactive with human and murine interleukin-7 - are useful  
XX for detecting and neutralising IL-7.  
XX  
PS Disclosure; Fig 5; 32pp; English.  
XX  
CC The present sequence represents human interleukin-7 (IL-7, also known as  
XX lymphopoietin-1 (LP-1) and pre-B cell growth factor). In addition to  
XX stimulating the development and proliferation of the hematopoietic  
XX precursors of T and B cells, IL-7 is also capable of inducing the  
XX proliferation of megakaryocyte and granulocyte/macrophage precursors in  
XX bone marrow. The mature protein is used to produce immunoreactive  
XX antibodies, particularly monoclonal antibodies. These antibodies are made  
XX by usual immunisation of mice with purified IL-7, then fusing their  
XX spleen cells with NS1 murine myeloma cells to produce antibody-secreting  
XX hybridomas. The antibodies are used to detect IL-7 and to neutralise it  
XX in assays or experiments involving many different lymphokines  
XX  
SQ Sequence 177 AA;

Query Match 100.0%; Score 922; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.6e-91;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60

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Db      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYSEVLMVSIIDQLDSMKEIGSNCL 60
Oy      61 NNEFFPFRKHICDANKEGMFLFPAARKLRQFLKKNSTGDFDLHLKXSEGTIILNCTGQ 120
        |||
Db      61 NNEFFPFRKHICDANKEGMFLFPAARKLRQFLKKNSTGDFDLHLKXSEGTIILNCTGQ 120
Oy      121 VKGRPALGEGAPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177
        |||
        121 VKGRPALGEGAPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177

RESULT 6
AAV41595
ID      AAV41595 standard; protein; 177 AA.
AC      AAV41595;
XX      18-JAN-2000 (first entry)
DT      18-JAN-2000 (first entry)
XX      Human interleukin-7 protein.
DE      Human interleukin-7; proliferation; megakaryocyte; granulocyte;
KW      Human; mouse; interleukin-7; proliferation; megakaryocyte; granulocyte;
        macrophage.
XX      Homo sapiens.
OS      US5965122-A.
PN      12-OCT-1999.
PD      12-OCT-1999.
XX      09-JUN-1997; 97US-00871161.
PF      26-OCT-1987; 87US-00113566.
XX      PR 07-OCT-1988; 88US-00255209.
XX      PR 13-APR-1990; 90US-00511438.
XX      PR 06-OCT-1992; 92US-00957649.
XX      PR 21-APR-1994; 94US-00231205.
XX      PR 22-MAY-1995; 95US-00446908.
XX      (SNFI ) SANOFI SA.
PA      Mochizuki DY, Lupton SD, Goodwin RG, Namen AE;
PI      WPI; 1999-579888/49.
XX      DR N-PSDB; AAZ30473.
XX      Inducing proliferation of hematopoietic cell precursors in a mammal.
PT      Example 3; Fig 5; 33pp; English.
PS      CC This sequence represents the human interleukin-7 protein. The invention
XX      CC relates to a new method for inducing the proliferation of megakaryocyte
XX      CC precursors or granulocyte/macrophage precursors in a mammal by
XX      CC administering to the mammal an effective amount of mammalian interleukin
XX      CC 7 (IL-7) in an admixture with a suitable diluent or carrier
XX      SQ Sequence 177 AA;

Query Match      100.0%; Score 922; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6e-91;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
AAB51092
ID      AAB51092 standard; protein; 177 AA.
AC      AAB51092;
XX      22-MAR-2001 (first entry)
DT      22-MAR-2001 (first entry)
XX      Human interleukin-7.
DE      Human; IL-7; immunomodulatory; lymphocyte development stimulator;
KW      immune response; interleukin-7.
XX      Homo sapiens.
OS      Key
XX      FH Key
XX      FT Peptide
XX      FT Peptide
XX      FT Protein
XX      Location/Qualifiers
XX      1..25
XX      /label= Signal_peptide
XX      26..177
XX      /label= Mature_protein
XX      US6156301-A.
XX      05-DEC-2000.
XX      12-MAY-1999; 99US-00310905.
XX      26-OCT-1987; 87US-00113566.
XX      PR 07-OCT-1988; 88US-00255209.
XX      PR 13-APR-1990; 90US-00511438.
XX      PR 06-OCT-1992; 92US-00957649.
XX      PR 21-APR-1994; 94US-00231205.
XX      PR 22-MAY-1995; 95US-00446908.
XX      PR 09-JUN-1997; 97US-00871161.
XX      (SNFI ) SANOFI-SYNTHELABO.
PA      Namen AE, Goodwin RG, Lupton SD, Mochizuki DY;
PI      WPI; 2001-090144/10.
XX      DR N-PSDB; AAF23611.
XX      Stimulating B or T lymphocyte development and proliferation or inducing
XX      PT proliferation of megakaryocyte precursors or granulocyte/macrophage in
XX      PT human comprises administering human interleukin-7.
XX      Claim 1; Fig 5; 33pp; English.
XX      CC The present sequence is human interleukin-7 (IL-7). IL-7 can be used to
XX      CC stimulate B or T lymphocyte development and proliferation, and to induce
XX      CC proliferation of megakaryocyte precursors or granulocyte/macrophage. In
XX      CC addition, IL-7 is useful for immune response augmentation
XX      SQ Sequence 177 AA;

Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6e-91;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
ABP59504
ID ABP59504 standard; protein; 177 AA.
XX
XX
AC ABP59504;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human interleukin-7 precursor protein.
XX
XX
KM Human; interleukin-7; IL-7; idiopathic pulmonary fibrosis.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200285300-A2.
XX
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US012814.
XX
XX
PR 23-APR-2001; 2001US-0285933P.
XX
XX
PR 24-APR-2001; 2001US-0286257P.
XX
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX
PI Huang M, Sharma S, Batra RK, Strieter RM, Dubinett SM, Keane MP;
XX
XX
WPI; 2003-093054/08.
XX
XX
PT Treating idiopathic pulmonary fibrosis in mammalian subject comprises
PT administering interleukin-7 polypeptide which inhibits transforming
PT growth factor beta production or signaling in a pulmonary fibrosis
PT fibroblast.
XX
XX
PS Claim 2; Page 42; 60pp; English.
XX
XX
CC The present invention relates to a method of treating idiopathic
CC pulmonary fibrosis (IPF) in a subject, comprising administering
CC interleukin-7 (IL-7) polypeptide, where the IL-7 polypeptide is capable
CC of inhibiting the transforming growth factor beta (TGF-beta) production,
CC or TGF-beta signaling in a interferon-gamma independent pathway, in a
CC pulmonary fibrosis fibroblast (PFB). The method is useful for treating
CC idiopathic pulmonary fibrosis in a mammalian subject. The present
CC sequence is the human IL-7 precursor protein
XX
XX
SQ Sequence 177 AA;

Query Match          100.0%; Score 922; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6e-91;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHHVSRRIYFGDLPRLIVLIPVASSDCDIEGDKGQYESVLMVSIQDLDSMKEIGSNCL 60
   |||||
DB 1 MHHVSFRRIYFGDLPRLIVLIPVASSDCDIEGDKGQYESVLMVSIQDLDSMKEIGSNCL 60
   |||||
QY 61 NNEFNPFKRHHICDANKEGMFLFPAARKLRQFLKMNSTGDPDLHLKVSBGTTILLNCTGQ 120
   |||||
DB 61 NNEFNPFKRHHICDANKEGMFLFPAARKLRQFLKMNSTGDPDLHLKVSBGTTILLNCTGQ 120
   |||||
QY 121 VNGRKPALGGAQPTKSLSEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTKEH 177
   |||||
DB 121 VNGRKPALGGAQPTKSLSEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTKEH 177
   |||||

RESULT 9
ADD05356
ID ADD05356 standard; protein; 177 AA.
XX
XX
AC ADD05356;
XX
XX
DT 01-JAN-2004 (first entry)
XX

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DE Human interleukin-7 (IL-7) polypeptide.
XX
XX
KM Human; interleukin-B50; IL-B50; immune disorder; T cell immunodeficiency;
KM chronic inflammation; tissue rejection; cardiovascular condition;
KM neurophysiological condition; antiinflammatory; immunosuppressive;
KM immunostimulant; cardiac; neuroprotective; interleukin-7; IL-7.
XX
XX
OS Homo sapiens.
XX
XX
PN US2003099947-A1.
XX
XX
PD 29-MAY-2003.
XX
XX
PF 25-SEP-2001; 2001US-00963347.
XX
XX
PR 21-SEP-1998; 98US-0101318P.
XX
XX
PR 27-APR-1998; 98US-0131298P.
XX
XX
PR 20-SEP-1999; 99US-00399492.
XX
XX
PA (BAZA/) BAZAN J F.
PA (MALE/) DE WAAL MALEFYT R.
PA (LIUY/) LIU Y.
PA (SOMU/) SOUMELIS V.
XX
XX
PI Bazan JF, De Waal Malefyt R, Liu Y, Soumelis V;
XX
XX
WPI; 2003-777307/73.
XX
XX
PT Novel isolated or recombinant polynucleotide encoding antigenic human
PT interleukin-B50 sequence which is useful for treating T cell
PT immunodeficiencies, chronic inflammation or tissue rejection, or
PT cardiovascular conditions.
XX
XX
PS Disclosure; SEQ ID NO 7; 54pp; English.
XX
XX
CC The invention relates to the human interleukin-B50 (IL-B50) polypeptide
CC and the polynucleotide encoding it. The polypeptide is useful for making
CC an antigenic polypeptide. The antigenic polypeptide is useful for binding
CC an antigen in a biological sample, where it forms a binding compound-
CC antigen complex. The polypeptide is also useful in forensic sciences to
CC distinguish rodent from human, or as a marker for distinguishing between
CC different cells exhibiting differential expression or modification
CC patterns. The sequences are useful for treating abnormal medical
CC conditions such as immune disorders e.g. T cell immunodeficiencies,
CC chronic inflammation or tissue rejection, or cardiovascular or
CC neurophysiological conditions. This sequence represents the human IL-7
CC polypeptide, which is homologous to the human IL-B50 polypeptide of the
CC invention.
XX
XX
SQ Sequence 177 AA;

Query Match          100.0%; Score 922; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6e-91;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHHVSRRIYFGDLPRLIVLIPVASSDCDIEGDKGQYESVLMVSIQDLDSMKEIGSNCL 60
   |||||
DB 1 MHHVSFRRIYFGDLPRLIVLIPVASSDCDIEGDKGQYESVLMVSIQDLDSMKEIGSNCL 60
   |||||
QY 61 NNEFNPFKRHHICDANKEGMFLFPAARKLRQFLKMNSTGDPDLHLKVSBGTTILLNCTGQ 120
   |||||
DB 61 NNEFNPFKRHHICDANKEGMFLFPAARKLRQFLKMNSTGDPDLHLKVSBGTTILLNCTGQ 120
   |||||
QY 121 VNGRKPALGGAQPTKSLSEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTKEH 177
   |||||
DB 121 VNGRKPALGGAQPTKSLSEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTKEH 177
   |||||

RESULT 10
ADC78857
ID ADC78857 standard; protein; 177 AA.
XX
XX
AC ADC78857;
XX

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XX 01-JAN-2004 (first entry)
XX Human PRO protein #43.
XX human; PRO: cancer; inflammatory bowel disease; ulcerative colitis;
XX Crohn's disease.
XX Homo sapiens.
XX MO2003034984-A2.
XX 01-MAY-2003.
XX 15-OCT-2002; 2002WO-US033070.
XX 19-OCT-2001; 2001US-0340083P.
XX (GETH ) GENENTECH INC.
XX Goddard A, Gurney AL;
XX WPI; 2003-481990/45.
XX N-PSDB; ADC78856.
XX New PRO polynucleotide and polypeptide, useful for the manufacture of a
XX medicament for diagnosing or treating cancer or inflammatory bowel
XX disorder e.g., ulcerative colitis or Crohn's disease.
XX Claim 12; SEQ ID NO 86; 327bp; English.
XX The invention comprises the amino acid and coding sequences of human PRO
XX proteins. The DNA and protein sequences of the invention are useful for
XX the diagnosis and treatment of cancer and inflammatory bowel disease
XX (e.g., ulcerative colitis or Crohn's disease). The present amino acid
XX sequence represents a human PRO protein of the invention.
XX Sequence 177 AA;
SQ
Query Match 100.0%; Score 922; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6e-91;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFHVSFRYIFGLPPLIVLVPVASSDCIEGKDGKQYESVLMVMSIDQLDSMKEIGSNCL 60
DB 1 MFHVSFRYIFGLPPLIVLVPVASSDCIEGKDGKQYESVLMVMSIDQLDSMKEIGSNCL 60
QY 61 NNEFNFPFRHICDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLILKVS EGTTLINCTGQ 120
DB 61 NNEFNFPFRHICDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLILKVS EGTTLINCTGQ 120
QY 121 VKGRKPALGEAQPTKSL EENKSLKEQKQKNDLCFLRLLOEIKTCWNKILMGTEKH 177
DB 121 VKGRKPALGEAQPTKSL EENKSLKEQKQKNDLCFLRLLOEIKTCWNKILMGTEKH 177
RESULT 11
ADF70851
ID ADF70851 standard; protein; 177 AA.
XX ADF70851;
XX 12-FEB-2004 (first entry)
XX Human interleukin 7 (IL-7).
XX immunostimulant; granulocyte macrophage colony stimulating factor;
XX GM-CSF; neutropenia; myelosuppressive chemotherapy;
XX bone marrow transplantation; HIV infection; burn; surgery; dilatation;
XX anaemia; neonatal septicemia; severe chronic neutropenia;
XX aplastic anaemia; acute leukaemia; human; growth hormone super family;
XX interleukin 7; IL-7.
XX
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```
OS Homo sapiens.
XX US2003171284-A1.
XX 11-SEP-2003.
XX 15-NOV-2002; 2002US-00298148.
XX 14-JUL-1997; 97US-0052516P.
XX PR 13-JUL-1998; 98WO-US014497.
XX PR 14-JAN-2000; 2000US-00462941.
XX PR 15-NOV-2001; 2001US-0332285P.
XX PR 11-OCT-2002; 2002US-0418040P.
XX (COXG/) COX G N.
XX (DOHE/) DOHERTY D H.
XX Cox GN, Doherty DH;
XX WPI; 2003-898295/82.
XX Protecting an animal from a disease or condition, useful for treating
XX neutropenia, comprises administering to an animal having the disease or
XX condition a composition comprising GM-CSF cysteine mutein.
XX Example 13; SEQ ID NO 14; 56bp; English.
XX The invention describes protecting an animal from a disease or condition
XX that can be treated by wild-type granulocyte macrophage colony
XX stimulating factor (GM-CSF) comprising administering to an animal having
XX the disease or condition a composition comprising GM-CSF cysteine mutein.
XX The methods are useful for preventing or treating the occurrence of
XX neutropenia in an animal, the neutropenia is selected from neutropenia
XX resulting from myelosuppressive chemotherapy, neutropenia associated with
XX bone marrow transplantation, neutropenia associated with infection with
XX the human immunodeficiency virus, neutropenia associated with burns,
XX surgery, dilatation, anaemia and neonatal septicemia, severe chronic
XX CC neutropenia, neutropenia associated with aplastic anaemia and acute
XX CC leukaemia. This is the amino acid sequence of human interleukin 7 (IL-7),
XX a member of the growth hormone super family which also includes GM-CSF.
XX Sequence 177 AA;
SQ
Query Match 100.0%; Score 922; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.6e-91;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFHVSFRYIFGLPPLIVLVPVASSDCIEGKDGKQYESVLMVMSIDQLDSMKEIGSNCL 60
DB 1 MFHVSFRYIFGLPPLIVLVPVASSDCIEGKDGKQYESVLMVMSIDQLDSMKEIGSNCL 60
QY 61 NNEFNFPFRHICDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLILKVS EGTTLINCTGQ 120
DB 61 NNEFNFPFRHICDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLILKVS EGTTLINCTGQ 120
QY 121 VKGRKPALGEAQPTKSL EENKSLKEQKQKNDLCFLRLLOEIKTCWNKILMGTEKH 177
DB 121 VKGRKPALGEAQPTKSL EENKSLKEQKQKNDLCFLRLLOEIKTCWNKILMGTEKH 177
RESULT 12
ADN95217
ID ADN95217 standard; protein; 177 AA.
XX ADN95217;
XX 01-JUL-2004 (first entry)
XX Human BEC/lEC-related protein sequence SegID139.
XX growth; differentiation; blood endothelial cell; BEC;
XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGF-R3;
XX lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cyostatic;
XX
```

KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;  
XX inflammatory disease; cancer metastasis; lymphatic system; human.  
OS Homo sapiens.  
XX WO2003080640-A1.  
XX PD 02-OCT-2003.  
XX 07-MAR-2003; 2003WO-US006900.  
XX PF 07-MAR-2002; 2002US-0363019P.  
XX PR 07-MAR-2002; 2002US-0363019P.  
XX (LUDM-) LUDMIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;  
XX DR WPI; 2003-876899/81.  
XX DR N-PSDB; ADN95218.  
XX PS Example 1; SEQ ID NO 139; 176pp; English.  
CC This invention relates to a method of differentially modulating the  
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic  
CC endothelial cells (LEC) comprises contacting endothelial cells with a  
CC composition comprising an agent that differentially modulates blood or  
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises  
CC identifying a human subject with lymphoedema and with a mutation in at  
CC least one allele of a gene encoding a LEC protein, where the mutation  
CC correlates with lymphoedema in human subjects, and with the proviso that  
CC the LEC protein is not VEGFR-3; and administering to the subject a  
CC composition comprising a lymphatic growth agent selected from VEGF-C or  
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for  
CC the development of compounds with an antiangiogenic, cytostatic,  
CC vasotropic or antiinflammatory activity or for gene therapy. The method  
CC is useful in modulating the growth or differentiation of blood  
CC endothelial cells or lymphatic endothelial cells, in treating hereditary  
CC lymphoedema, in screening for an endothelial cell disorder or  
CC predisposition to the disorder or in monitoring the efficacy or toxicity  
CC of a drug on endothelial cells. The agent is useful in manufacturing a  
CC medicament for the differential modulation of blood vessel endothelial  
CC cell or lymphatic vessel endothelial cell growth or differentiation. The  
CC lymphatic growth agent may also be used in manufacturing a medicament for  
CC the treatment of hereditary lymphoedema resulting from a mutation in a  
CC LEC gene or of other diseases involving the lymphatic vessels, such as  
CC various inflammatory diseases and cancer metastasis via the lymphatic  
CC system. The present sequence is that of a human LEC/BEC differentially  
CC expressed protein which is related to the method of the invention. Note:  
CC This sequence does not appear in the specification but was obtained by  
CC the indexer using the source data given in table 14 of the specification.  
XX SQ Sequence 177 AA;  
Query Match 100.0%; Score 922; DB 7; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.6e-91;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEFVSRFYFGPLPILVLLPVASSDSDIEGKDGKQYSEVLMWSIDOLDSMKEIGSNCL 60  
DB 1 MEFVSRFYFGPLPILVLLPVASSDSDIEGKDGKQYSEVLMWSIDOLDSMKEIGSNCL 60  
QY 61 NNEFNFKKHICDANEGMFLPAARKLOPKMNSGTGPDHLVSGTTLINCTQO 120  
DB 61 NNEFNFKKHICDANEGMFLPAARKLOPKMNSGTGPDHLVSGTTLINCTQO 120  
QY 121 VKGRRPALGEAQPSTSLSEKSLKEOKLNDLCFLKRLLOEITKQWNKILMGTKKH 177  
DB 121 VKGRRPALGEAQPSTSLSEKSLKEOKLNDLCFLKRLLOEITKQWNKILMGTKKH 177  
RESULT 13  
ADM11079

ID ADM11079 standard; protein; 177 AA.  
XX AC ADM11079;  
XX DT 20-MAY-2004 (first entry)  
XX DE Recombinant human IL-7 conformer protein SEQ ID NO:4.  
XX KW interleukin 7 conformer; IL-7 conformer; disulfide bridge;  
XX KW immunostimulant; B lymphocyte development; T lymphocyte development;  
XX KW B lymphocyte proliferation; T lymphocyte proliferation; immune response;  
XX KW infection; immunodeficient; lymphoproliferation; cancer; human.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO2004018681-A2.  
XX PD 04-MAR-2004.  
XX PF 06-AUG-2003; 2003WO-EP008701.  
XX PR 08-AUG-2002; 2002EP-00291996.  
XX PR 05-JUN-2003; 2003US-0475881P.  
XX PA (CYTH-) CYTHERIS.  
XX PI Morre MC, Aseouline B, Cortez P, Gregoire A;  
XX DR WPI; 2004-226853/21.  
XX DR N-PSDB; ADM11078.  
XX PT New purified or isolated IL-7 conformer comprising three disulfide  
XX PT bridges, useful for preventing or reducing opportunistic infections in  
XX PT immunodeficient patients, cancer patients, patients undergoing grafts.  
XX PS Claim 3; SEQ ID NO 4; 110pp; English.  
CC The present invention describes a purified or isolated interleukin 7 (IL-  
CC 7) conformer comprising three disulfide bridges: (i) Cys: 1-4 (Cys2-  
CC Cys92); (ii) 2-5 (Cys34-Cys129); and (iii) 3-6 (Cys47-Cys141). Also  
CC described: (1) an IL-7 drug substance comprising, as the desired product,  
CC the IL-7 conformer, where the drug substance is substantially free of IL-  
CC 7 molecular variants or product related impurities, and where the total  
CC amount of weight of IL-7 in the drug substance is at least 98, preferably  
CC 99.5 % by weight; (2) a pharmaceutical composition comprising the drug  
CC substance and one or more carriers; (3) a nucleic acid molecule encoding  
CC the IL-7 polypeptide, where the molecule comprises an altered Shine-  
CC Dalgarno-like sequence; (4) a vector comprising the nucleic acid; (5) a  
CC recombinant host cell comprising the nucleic acid or the vector; (6) an  
CC antibody specifically immunoreactive with the IL-7 conformer; (7) a  
CC method of producing an IL-7 drug substance or pharmaceutical composition;  
CC and (8) a method of controlling an IL-7 containing preparation by  
CC determining the presence and/or relative quantity, in the preparation, of  
CC an IL-7 conformer. IL-7 conformer has immunostimulant activity. The  
CC conformer and pharmaceutical composition are useful for prophylactic or  
CC therapeutic stimulation of B or T lymphocyte development and  
CC proliferation, or for enhancement of global or specific immuno-  
CC reconstitution, or for enhancement of humoral or cellular immune  
CC response. They are also useful for preventing or reducing opportunistic  
CC infections in immunodeficient patients; for prolonging lymphoproliferation  
CC stimulation and/or producing specific immune response and/or to broaden  
CC the repertoire of a specific immune response in human patients, e.g.,  
CC immunodeficient patients, cancer patients, patients undergoing grafts,  
CC patients infected with a virus or a parasite, elderly patients or any  
CC recombinant human IL-7 conformer. The present sequence represents a  
CC the present invention.  
XX SQ Sequence 177 AA;  
Query Match 100.0%; Score 922; DB 8; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.6e-91;

Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cc 1 MFHVSFRYIFGLPLILVILPVASSDCDIEGDKQKQYEVLMVSIIDQLDSMKEIGSNCL 60  
Db 1 MFHVSFRYIFGLPLILVILPVASSDCDIEGDKQKQYEVLMVSIIDQLDSMKEIGSNCL 60

Qy 61 NNEFNPFKRHI CDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLKXVSEGTILLNCTGQ 120  
Cc 61 NNEFNPFKRHI CDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLKXVSEGTILLNCTGQ 120  
Db 61 NNEFNPFKRHI CDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLKXVSEGTILLNCTGQ 120

Qy 121 VKGRKPAALGEAQPTKSLIENKSLKEOKKNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
Cc 121 VKGRKPAALGEAQPTKSLIENKSLKEOKKNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
Db 121 VKGRKPAALGEAQPTKSLIENKSLKEOKKNDLCFLKRLLOEIKTCWNKILMGTEKH 177

RESULT 14  
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ID ADM11101 standard; protein; 177 AA.  
AC ADM11101;  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Human interleukin 7 amino acid sequence.  
DE  
XX  
XX interleukin 7 conformer; IL-7 conformer; disulfide bridge;  
KW immunostimulant; B lymphocyte development; T lymphocyte development;  
KW B lymphocyte proliferation; T lymphocyte proliferation; immune response;  
KW infection; immunodeficient; lymphoproliferation; cancer; human.  
XX  
XX Homo sapiens.  
OS  
XX WO2004018681-A2.  
XX  
XX 04-MAR-2004.  
PD  
XX 06-AUG-2003; 2003WO-EP008701.  
PF  
XX 08-AUG-2002; 2002EP-00291996.  
PR 05-JUN-2003; 2003US-0475881P.  
XX  
XX (CYTH-) CYTHERIS.  
PA  
XX Morre MC, Assouline B, Cortez P, Gregoire A;  
PI  
XX WPI, 2004-226853/21.  
XX  
XX  
XX New purified or isolated IL-7 conformer comprising three disulfide  
PT bridges, useful for preventing or reducing opportunistic infections in  
PT immunodeficient patients, cancer patients, patients undergoing grafts.  
XX  
XX Example A; Fig 5; 110pp; English.

The present invention describes a purified or isolated interleukin 7 (IL-7) conformer comprising three disulfide bridges: (1) Cys: 1-4 (Cys2-Cys92); (1i) 2-5 (Cys34-Cys129); and (1ii) 3-6 (Cys47-Cys141). Also described: (1) an IL-7 drug substance comprising, as the desired product, the IL-7 conformer, where the drug substance is substantially free of IL-7 molecular variants or product related impurities, and where the total amount of weight of IL-7 in the drug substance is at least 98, preferably 99.5 % by weight; (2) a pharmaceutical composition comprising the drug substance and one or more carriers; (3) a nucleic acid molecule encoding the IL-7 polypeptide, where the molecule comprises an altered Shine-Dalgarno-like sequence; (4) a vector comprising the nucleic acid; (5) a recombinant host cell comprising the nucleic acid or the vector; (6) an antibody specifically immunoreactive with the IL-7 conformer; (7) a method of producing an IL-7 drug substance or pharmaceutical composition; and (8) a method of controlling an IL-7 containing preparation by determining the presence and/or relative quantity, in the preparation, of an IL-7 conformer. IL-7 conformer has immunostimulant activity. The conformer and pharmaceutical composition are useful for prophylactic or therapeutic stimulation of B or T lymphocyte development and proliferation, or for enhancement of global or specific immuno-

reconstitution, or for enhancement of humoral or cellular immune response. They are also useful for preventing or reducing opportunistic infections in immunodeficient patients; for prolonging lymphoproliferation and/or producing specific immune response and/or to broaden the repertoire of a specific immune response in human patients, e.g. immunodeficient patients, cancer patients, patients undergoing grafts, patients infected with a virus or a parasite, elderly patients or any patients having low CD4 count. The present sequence represents a human IL-7 amino acid sequence, which is used in the exemplification of the present invention.

Sequence 177 AA:  
SQ  
Query Match 100.0%; Score 922; DB 8; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.6e-91;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFHVSFRYIFGLPLILVILPVASSDCDIEGDKQKQYEVLMVSIIDQLDSMKEIGSNCL 60  
Cc 1 MFHVSFRYIFGLPLILVILPVASSDCDIEGDKQKQYEVLMVSIIDQLDSMKEIGSNCL 60  
Db 1 MFHVSFRYIFGLPLILVILPVASSDCDIEGDKQKQYEVLMVSIIDQLDSMKEIGSNCL 60

Qy 61 NNEFNPFKRHI CDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLKXVSEGTILLNCTGQ 120  
Cc 61 NNEFNPFKRHI CDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLKXVSEGTILLNCTGQ 120  
Db 61 NNEFNPFKRHI CDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLKXVSEGTILLNCTGQ 120

Qy 121 VKGRKPAALGEAQPTKSLIENKSLKEOKKNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
Cc 121 VKGRKPAALGEAQPTKSLIENKSLKEOKKNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
Db 121 VKGRKPAALGEAQPTKSLIENKSLKEOKKNDLCFLKRLLOEIKTCWNKILMGTEKH 177

RESULT 15  
ADO50323  
ID ADO50323 standard; protein; 177 AA.  
AC ADO50323;  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Human IL-7.  
DE  
XX  
XX Cytokine; interleukin-B50; IL-B50; differentiation; haematopoietic cell;  
KW immune disorder; T cell immune deficiency; chronic inflammation;  
KW tissue rejection; cardiovascular; neurophysiological; antigen; immunogen;  
KW IL-7; human.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
XX Key Location/Qualifiers  
FT Modified-site 95  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 116  
FT Modified-site /note= "N-glycosylated"  
XX  
XX US2004091970-A1.  
XX  
XX 13-MAY-2004.  
XX  
XX 20-JUN-2003; 2003US-00601105.  
XX  
XX 21-SEP-1998; 98US-0101318P.  
XX 27-APR-1999; 99US-0131298P.  
XX 20-SEP-1999; 99US-00399492.  
XX 25-SEP-2001; 2001US-00963347.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Bazan JF, De Waal Malefyt R, Liu Y, Soumeijs V;  
XX WPI, 2004-374953/35.  
XX  
XX Novel isolated or recombinant polynucleotide such as cytokine e.g., IL-7  
PT B50 useful for producing an antigenic polypeptide, for treating T cell  
PT immune deficiencies, chronic inflammation, tissue rejection or





**This Page Blank (uspto)**

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OM protein - protein search, using sw model

Run on: December 29, 2005, 14:21:14 ; Search time 163 seconds  
(without alignments)  
453.717 Million cell updates/sec

Title: US-10-706-801-1

Perfect score: 922

Sequence: 1 MFHVSFRYIFGLPPLILVL.....RLDRIKTCWNKILMGTEKH 177

Scoring table:

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	922	100.0	177	3	US-09-963-347B-7 Sequence 7, Appli
2	922	100.0	177	4	US-10-400-377-14 Sequence 14, Appl
3	922	100.0	177	4	US-10-400-708-14 Sequence 14, Appl
4	922	100.0	177	4	US-10-298-148-14 Sequence 14, Appl
5	922	100.0	177	4	US-10-601-105-7 Sequence 7, Appli
6	922	100.0	177	4	US-10-773-939-14 Sequence 14, Appl
7	922	100.0	177	4	US-10-774-149-14 Sequence 14, Appl
8	922	100.0	177	4	US-10-773-654-14 Sequence 14, Appl
9	922	100.0	177	5	US-10-866-540-14 Sequence 14, Appl
10	922	100.0	177	5	US-10-688-845-8 Sequence 8, Appli
11	922	100.0	177	5	US-10-856-219-14 Sequence 14, Appl
12	922	100.0	177	5	US-10-706-801-1 Sequence 1, Appli
13	922	100.0	177	5	US-10-685-288-14 Sequence 14, Appl
14	922	100.0	177	5	US-10-491-997-86 Sequence 86, Appl
15	922	100.0	177	5	US-10-866-580-14 Sequence 14, Appl
16	922	100.0	177	6	US-11-027-446-1 Sequence 1, Appli
17	922	100.0	177	6	US-11-027-446-1 Sequence 14, Appl
18	922	100.0	177	6	US-11-071-098-14 Sequence 14, Appl
19	922	100.0	177	6	US-11-070-993-14 Sequence 14, Appl
20	922	100.0	345	5	US-10-895-396-1 Sequence 1, Appli
21	800	86.8	398	6	US-11-027-446-6 Sequence 6, Appli
22	797	86.4	383	6	US-11-027-446-5 Sequence 5, Appli
23	797	86.4	384	6	US-11-027-446-4 Sequence 8, Appli
24	796	86.3	391	6	US-11-027-446-7 Sequence 7, Appli
25	796	86.3	393	6	US-11-027-446-7 Sequence 13, Appl
26	717	77.8	157	5	US-10-764-833-13 Sequence 9, Appli
27	715	77.5	167	5	US-10-764-833-9

28	679.5	73.7	176	3	US-09-963-347B-5	Sequence 5, Appli
29	679.5	73.7	176	4	US-10-601-105-5	Sequence 5, Appli
30	679.5	73.7	176	6	US-11-027-446-3	Sequence 3, Appli
31	677.5	73.5	176	3	US-09-963-347B-6	Sequence 6, Appli
32	677.5	73.5	176	4	US-10-601-105-6	Sequence 6, Appli
33	671.5	72.8	176	6	US-11-027-446-2	Sequence 2, Appli
34	536.5	58.2	154	4	US-09-963-347B-8	Sequence 8, Appli
35	536.5	58.2	154	4	US-10-601-105-8	Sequence 8, Appli
36	536.5	58.2	333	5	US-10-963-396-2	Sequence 2, Appli
37	528.5	57.3	154	3	US-09-963-347B-9	Sequence 9, Appli
38	528.5	57.3	154	4	US-10-601-105-9	Sequence 9, Appli
39	140.5	15.2	280	3	US-09-365-940-23	Sequence 23, Appl
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41	140.5	15.2	280	4	US-10-200-242-23	Sequence 23, Appl
42	137.5	14.9	216	5	US-10-473-127-260	Sequence 260, App
43	137.5	14.9	216	5	US-10-473-127-261	Sequence 261, App
44	136.5	14.8	273	3	US-09-365-940-21	Sequence 21, Appl
45	136.5	14.8	273	4	US-10-200-242-21	Sequence 21, Appl

#### ALIGNMENTS

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RESULT 1
US-09-963-347B-7
; Sequence 7, Application US/09963347B
; Publication No. US20030099947A1
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Liu, Yong-Jun
; APPLICANT: Soumellis, Vassili
; TITLE OF INVENTION: MAMMALIAN CYTOKINES, RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0903K1
; CURRENT APPLICATION NUMBER: US/09/963,347B
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/399,492
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: US 60/131,298
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: US 60/101,318
; PRIOR FILING DATE: 1998-09-21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-347B-7
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Best Local Similarity 100.0%; Pred. No. 4.9e-92; Indels 0; Gaps 0;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MFHVSFRYIFGLPPLILVLPAVSSDCIEGDKGQYBSVLMVNSIDQLDSMKEIGSNCL 60
        1 MFHVSFRYIFGLPPLILVLPAVSSDCIEGDKGQYBSVLMVNSIDQLDSMKEIGSNCL 60
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DB      61 NNEFFPRGHICDANKKEGMLFRARKKIROPLKKNSTGDFDLHLKVSRGITILLNCTGQ 120
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        121 VKGRPALGSAQPTKSLSEENKSLKEOKKLDLCTFKRLDRIKTCWNKILMGTEKH 177
DB      121 VKGRPALGSAQPTKSLSEENKSLKEOKKLDLCTFKRLDRIKTCWNKILMGTEKH 177
        121 VKGRPALGSAQPTKSLSEENKSLKEOKKLDLCTFKRLDRIKTCWNKILMGTEKH 177

RESULT 2
US-10-400-377-14
; Sequence 14, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
```

```
APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-14
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Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MFHVSFRITFGILPPLILVLVPVASSDCDIEGKDGQYESSVLMWSIDQLLDSMKEIGSNCL 60
QY 61 NNEFNFFKRHI CDANKEGMFLFRAARKLRQFLKNNSTGDFDLHLKVS EGTTLINCTGQ 120
DB 61 NNEFNFFKRHI CDANKEGMFLFRAARKLRQFLKNNSTGDFDLHLKVS EGTTLINCTGQ 120
QY 121 VKGRKPALGGAQPTKSL EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTKEH 177
DB 121 VKGRKPALGGAQPTKSL EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTKEH 177
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## RESULT 3

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US-10-400-708-14
; Sequence 14, Application US/10400708
; Publication No. US2003016685A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-14
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Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MFHVSFRITFGILPPLILVLVPVASSDCDIEGKDGQYESSVLMWSIDQLLDSMKEIGSNCL 60
DB 1 MFHVSFRITFGILPPLILVLVPVASSDCDIEGKDGQYESSVLMWSIDQLLDSMKEIGSNCL 60
QY 61 NNEFNFFKRHI CDANKEGMFLFRAARKLRQFLKNNSTGDFDLHLKVS EGTTLINCTGQ 120
DB 61 NNEFNFFKRHI CDANKEGMFLFRAARKLRQFLKNNSTGDFDLHLKVS EGTTLINCTGQ 120
QY 121 VKGRKPALGGAQPTKSL EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTKEH 177
DB 121 VKGRKPALGGAQPTKSL EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTKEH 177
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```
RESULT 4
US-10-298-148-14
; Sequence 14, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-14
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Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MFHVSFRITFGILPPLILVLVPVASSDCDIEGKDGQYESSVLMWSIDQLLDSMKEIGSNCL 60
DB 1 MFHVSFRITFGILPPLILVLVPVASSDCDIEGKDGQYESSVLMWSIDQLLDSMKEIGSNCL 60
QY 61 NNEFNFFKRHI CDANKEGMFLFRAARKLRQFLKNNSTGDFDLHLKVS EGTTLINCTGQ 120
DB 61 NNEFNFFKRHI CDANKEGMFLFRAARKLRQFLKNNSTGDFDLHLKVS EGTTLINCTGQ 120
QY 121 VKGRKPALGGAQPTKSL EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTKEH 177
DB 121 VKGRKPALGGAQPTKSL EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTKEH 177
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## RESULT 5

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US-10-601-105-7
; Sequence 7, Application US/10601105
; Publication No. US20040091970A1
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Liu, Yong-Jun
; APPLICANT: Soumelis, Vassili
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0903K1
; CURRENT APPLICATION NUMBER: US/10/601,105
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/963,347B
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/399,492
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: US 60/131,298
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: US 60/101,318
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-105-7
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Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy		1	MHVSFRIYFGPPLILVLLPVASSDCDIEGDKQGYEBSVLWWSIDQLDSMKEIGSNCL	60
Dd		1	MHVSFRIYFGPPLILVLLPVASSDCDIEGDKQGYEBSVLWWSIDQLDSMKEIGSNCL	60
Oy		61	NNEFNFRKHICDANKEGMFLEFRARKLRQFLKMNSTGDFDLHLKVSEGTILLNCTQG	120
Dd		61	NNEFNFRKHICDANKEGMFLEFRARKLRQFLKMNSTGDFDLHLKVSEGTILLNCTQG	120
Oy		121	VKGRRPALGEAQPFTKSLEENSKLKEOKKLNDLCFLKRLLOEIKTCWNKILMGTEKH	177
Dd		121	VKGRRPALGEAQPFTKSLEENSKLKEOKKLNDLCFLKRLLOEIKTCWNKILMGTEKH	177

  

RESULT 6

US-10-773-939-14

/ Sequence 14, Application US/10773939  
 / Publication No. US20040175356A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Cox III, George N  
 / APPLICANT: Bolder Biotechnology, Inc.  
 / TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins  
 / FILE REFERENCE: 4152-1-PUS  
 / CURRENT APPLICATION NUMBER: US/10/773, 939  
 / CURRENT FILING DATE: 2004-02-05  
 / PRIOR APPLICATION NUMBER: US/10/400, 377  
 / PRIOR FILING DATE: 2003-03-26  
 / PRIOR APPLICATION NUMBER: US/09/462, 941  
 / PRIOR FILING DATE: 2000-01-14  
 / PRIOR APPLICATION NUMBER: 60/052, 516  
 / PRIOR FILING DATE: 1997-07-14  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO 14  
 / LENGTH: 177  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-773-939-14

Query Match	100.0%	Score 922;	DB 4;	Length 177;
Best Local Similarity	100.0%;	Pred. No.	4.9e-92;	
Matches 177; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

  

Oy		1	MHVSFRIYFGPPLILVLLPVASSDCDIEGDKQGYEBSVLWWSIDQLDSMKEIGSNCL	60
Dd		1	MHVSFRIYFGPPLILVLLPVASSDCDIEGDKQGYEBSVLWWSIDQLDSMKEIGSNCL	60
Oy		61	NNEFNFRKHICDANKEGMFLEFRARKLRQFLKMNSTGDFDLHLKVSEGTILLNCTQG	120
Dd		61	NNEFNFRKHICDANKEGMFLEFRARKLRQFLKMNSTGDFDLHLKVSEGTILLNCTQG	120
Oy		121	VKGRRPALGEAQPFTKSLEENSKLKEOKKLNDLCFLKRLLOEIKTCWNKILMGTEKH	177
Dd		121	VKGRRPALGEAQPFTKSLEENSKLKEOKKLNDLCFLKRLLOEIKTCWNKILMGTEKH	177

  

RESULT 7

US-10-774-149-14

/ Sequence 14, Application US/10774149  
 / Publication No. US20040175800A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Cox III, George N  
 / APPLICANT: Bolder Biotechnology, Inc.  
 / TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins  
 / FILE REFERENCE: 4152-1-PUS  
 / CURRENT APPLICATION NUMBER: US/10/774, 149  
 / CURRENT FILING DATE: 2004-02-05  
 / PRIOR APPLICATION NUMBER: US/10/400, 377  
 / PRIOR FILING DATE: 2003-03-26  
 / PRIOR APPLICATION NUMBER: US/09/462, 941  
 / PRIOR FILING DATE: 2000-01-14  
 / PRIOR APPLICATION NUMBER: 60/052, 516  
 / PRIOR FILING DATE: 1997-07-14

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; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-774-149-14

Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  MEHVSFRYIGLPELLIIVLTPVASSDDIEGKQKQYESVLMVSIIDQLDSMKRIGSNCL 60
DB      1  MEHVSFRYIGLPELLIIVLTPVASSDDIEGKQKQYESVLMVSIIDQLDSMKRIGSNCL 60

OY      61  NNEENPFRRHICDANKGEMFLFRAARKLRQPLKNNSTGDPDLHLIKVSEGTIILLNCTGQ 120
DB      61  NNEENPFRRHICDANKGEMFLFRAARKLRQPLKNNSTGDPDLHLIKVSEGTIILLNCTGQ 120

OY      121 VKGRKPAALGEAQTSLSEENKSLKEQKLANDLCLFKRLLOEITKCNKILMGTEKH 177
DB      121 VKGRKPAALGEAQTSLSEENKSLKEQKLANDLCLFKRLLOEITKCNKILMGTEKH 177

RESULT 8
US-10-773-654-14
; Sequence 14, Application US/10773654
; Publication No. US20040214287A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,654
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-654-14

Query Match      100.0%; Score 922; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  MEHVSFRYIGLPELLIIVLTPVASSDDIEGKQKQYESVLMVSIIDQLDSMKRIGSNCL 60
DB      1  MEHVSFRYIGLPELLIIVLTPVASSDDIEGKQKQYESVLMVSIIDQLDSMKRIGSNCL 60

OY      61  NNEENPFRRHICDANKGEMFLFRAARKLRQPLKNNSTGDPDLHLIKVSEGTIILLNCTGQ 120
DB      61  NNEENPFRRHICDANKGEMFLFRAARKLRQPLKNNSTGDPDLHLIKVSEGTIILLNCTGQ 120

OY      121 VKGRKPAALGEAQTSLSEENKSLKEQKLANDLCLFKRLLOEITKCNKILMGTEKH 177
DB      121 VKGRKPAALGEAQTSLSEENKSLKEQKLANDLCLFKRLLOEITKCNKILMGTEKH 177

RESULT 9
US-10-866-540-14
; Sequence 14, Application US/10866540
; Publication No. US20040230040A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N

```

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; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/866,540
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-866-540-14
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Query Match          100.0%; Score 922; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
        |||
        1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
DB
QY      61 NNEFNFPRRHICDANKEGMFLFRARKLRQPLKMNSTGDPDLHLKXVSEGTIILNCTGQ 120
        |||
        61 NNEFNFPRRHICDANKEGMFLFRARKLRQPLKMNSTGDPDLHLKXVSEGTIILNCTGQ 120
DB
QY      121 VKGRPPALGEGAQPTKSLSEENKSLKEQKNDLCLFKRLLOEIKTCWNKILMGTEKH 177
        |||
        121 VKGRPPALGEGAQPTKSLSEENKSLKEQKNDLCLFKRLLOEIKTCWNKILMGTEKH 177
DB
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RESULT 10
US-10-688-845-8
; Sequence 8, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
; APPLICANT: Lotze, Michael T
; APPLICANT: Tahara, Hideaki
; TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
; FILE REFERENCE: UPT-004
; CURRENT APPLICATION NUMBER: US/10/688,845
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,865
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-845-8
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Query Match          100.0%; Score 922; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
        |||
        1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
DB
QY      61 NNEFNFPRRHICDANKEGMFLFRARKLRQPLKMNSTGDPDLHLKXVSEGTIILNCTGQ 120
        |||
        61 NNEFNFPRRHICDANKEGMFLFRARKLRQPLKMNSTGDPDLHLKXVSEGTIILNCTGQ 120
DB
QY      121 VKGRPPALGEGAQPTKSLSEENKSLKEQKNDLCLFKRLLOEIKTCWNKILMGTEKH 177
        |||
        121 VKGRPPALGEGAQPTKSLSEENKSLKEQKNDLCLFKRLLOEIKTCWNKILMGTEKH 177
DB
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RESULT 11
US-10-856-219-14
; Sequence 14, Application US/10856219
; Publication No. US20040265269A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/856,219
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-856-219-14
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Query Match          100.0%; Score 922; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
        |||
        1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
DB
QY      61 NNEFNFPRRHICDANKEGMFLFRARKLRQPLKMNSTGDPDLHLKXVSEGTIILNCTGQ 120
        |||
        61 NNEFNFPRRHICDANKEGMFLFRARKLRQPLKMNSTGDPDLHLKXVSEGTIILNCTGQ 120
DB
QY      121 VKGRPPALGEGAQPTKSLSEENKSLKEQKNDLCLFKRLLOEIKTCWNKILMGTEKH 177
        |||
        121 VKGRPPALGEGAQPTKSLSEENKSLKEQKNDLCLFKRLLOEIKTCWNKILMGTEKH 177
DB
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RESULT 12
US-10-706-801-1
; Sequence 1, Application US/10706801
; Publication No. US20050054054A1
; GENERAL INFORMATION:
; APPLICANT: Foss, Francine M.
; APPLICANT: Cosenza, Larry
; TITLE OF INVENTION: INTERLEUKIN-7 MOLECULES WITH ALTERED
; FILE REFERENCE: 00398-152001
; CURRENT APPLICATION NUMBER: US/10/706,801
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/425,925
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-801-1
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Query Match          100.0%; Score 922; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
        |||
        1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQYVESVLMVSIIDQLDSMKEIGSNCL 60
DB
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QY 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
QY 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177

## RESULT 13

US-10-685-288-14  
Sequence 14, Application US/10685288  
Publication No. US20050058621A1  
GENERAL INFORMATION:

APPLICANT: Bolder Biotechnology, Inc.  
APPLICANT: Cox III, George N  
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins, and Methods of  
FILE REFERENCE: 4152-1-PUS-8  
CURRENT APPLICATION NUMBER: US/10/685,288  
CURRENT FILING DATE: 2003-10-13  
PRIOR APPLICATION NUMBER: 60/418,106  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: 60/418,105  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: 10/400,377  
PRIOR FILING DATE: 2003-03-26  
PRIOR APPLICATION NUMBER: 09/462,941  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: PCT/US98/14497  
PRIOR FILING DATE: 1998-07-13  
PRIOR APPLICATION NUMBER: 60/052,516  
PRIOR FILING DATE: 1997-07-14  
PRIOR APPLICATION NUMBER: 10/298,148  
PRIOR FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: 60/418,040  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: 60/332,285  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 09/889,273  
PRIOR FILING DATE: 2001-07-13  
Remaining Prior Application data removed - See File Wrapper or PAM.  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-685-288-14

Query Match 100.0%; Score 922; DB 5; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.9e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHHVSFRYIFGLPPLILVLLPVASSDCDIEGKGQYSESVLMVSIIDQLDSMKEIGSNCL 60  
DB 1 MHHVSFRYIFGLPPLILVLLPVASSDCDIEGKGQYSESVLMVSIIDQLDSMKEIGSNCL 60  
QY 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
QY 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177

## RESULT 14

US-10-491-997-86  
Sequence 86, Application US/10491997  
Publication No. US2005008957A1  
GENERAL INFORMATION:  
APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF INFLAMMATORY BOWEL DISORDERS  
FILE REFERENCE: P1915R1 US

CURRENT APPLICATION NUMBER: US/10/491,997  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: PCT/US02/33070  
PRIOR FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: US 60/340,083  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 162  
SEQ ID NO 86  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-491-997-86

Query Match 100.0%; Score 922; DB 5; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.9e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHHVSFRYIFGLPPLILVLLPVASSDCDIEGKGQYSESVLMVSIIDQLDSMKEIGSNCL 60  
DB 1 MHHVSFRYIFGLPPLILVLLPVASSDCDIEGKGQYSESVLMVSIIDQLDSMKEIGSNCL 60  
QY 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
QY 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177

## RESULT 15

US-10-866-580-14  
Sequence 14, Application US/10866580  
Publication No. US20050096461A1  
GENERAL INFORMATION:

APPLICANT: Bolder Biotechnology, Inc.  
APPLICANT: Cox III, George N  
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins  
FILE REFERENCE: 4152-1-PUS  
CURRENT APPLICATION NUMBER: US/10/866,580  
CURRENT FILING DATE: 2004-06-10  
PRIOR APPLICATION NUMBER: US/10/400,377  
PRIOR FILING DATE: 2003-03-26  
PRIOR APPLICATION NUMBER: US/09/462,941  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: 60/052,516  
PRIOR FILING DATE: 1997-07-14  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-866-580-14

Query Match 100.0%; Score 922; DB 5; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.9e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHHVSFRYIFGLPPLILVLLPVASSDCDIEGKGQYSESVLMVSIIDQLDSMKEIGSNCL 60  
DB 1 MHHVSFRYIFGLPPLILVLLPVASSDCDIEGKGQYSESVLMVSIIDQLDSMKEIGSNCL 60  
QY 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFNFRKHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
QY 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VGRKPAALGEAQPYSLEENKSLKEOKKLANDLCLFKRLLOEIKTCWNKILMGTEKH 177

Db 121 VKGRPAALGEAOPTKSLEENKSLKEQKNDLCFLKRLQEIKTQWKNKILMGTEH 177

Search completed: December 29, 2005, 14:35:23  
Job time : 164 secs

---



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2005, 14:21:54 ; Search time 13 Seconds  
(without alignments)  
101.965 Million cell updates/sec

Title: US-10-706-801-1  
Perfect score: 922  
Sequence: 1 MFHVSFRYIFGHPPLILVLL.....RLDGIKTCWNKILMGTEKH 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
1: /cgn2\_6/prodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubppaa/US11\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/2/pubppaa/US12\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	922	100.0	177	6	US-10-522-883-4
2	895	97.1	177	6	US-10-522-883-13
3	815	86.4	173	6	US-10-522-883-19
4	800.5	86.8	179	6	US-10-522-883-17
5	796	86.3	153	6	US-10-522-883-2
6	788	85.5	173	6	US-10-522-883-23
7	773.5	83.9	179	6	US-10-522-883-21
8	77.5	8.4	741	7	US-11-191-374-18
9	77.5	8.4	741	7	US-11-191-375-18
10	77.5	8.4	741	7	US-11-191-588-18
11	75.5	8.2	742	7	US-11-191-374-46
12	75.5	8.2	742	7	US-11-191-375-46
13	75.5	8.2	742	7	US-11-191-588-46
14	73	7.9	612	6	US-10-467-657-3988
15	72.5	7.9	291	7	US-11-102-883-22
16	69	7.5	317	6	US-10-821-234-1388
17	68.5	7.4	450	6	US-10-995-561-815
18	68	7.4	292	7	US-11-102-883-24
19	67.5	7.3	733	7	US-11-012-762-68
20	67	7.3	167	6	US-10-467-657-2942
21	66.5	7.2	1045	7	US-11-055-822-100
22	66.5	7.2	1049	7	US-11-137-465-42
23	66	7.2	1299	6	US-10-821-234-1145
24	64	6.9	446	6	US-10-793-626-2250
25	64	6.9	752	6	US-10-793-626-1036

26	64	6.9	792	7	US-11-108-172-1127	Sequence 1127, Ap
27	64	6.9	1404	6	US-10-878-556A-169	Sequence 169, App
28	63.5	6.9	325	6	US-10-793-626-1076	Sequence 1076, Ap
29	63.5	6.9	659	6	US-10-995-561-573	Sequence 573, App
30	63.5	6.9	701	6	US-10-995-561-575	Sequence 575, App
31	63.5	6.9	751	6	US-10-995-561-578	Sequence 578, App
32	63.5	6.9	808	6	US-10-995-561-574	Sequence 574, App
33	63.5	6.9	808	6	US-11-105-268-53	Sequence 53, App
34	63	6.8	296	7	US-11-196-475-122	Sequence 122, App
35	63	6.8	350	7	US-11-149-349-8	Sequence 8, App
36	63	6.8	380	7	US-11-196-475-118	Sequence 118, App
37	63	6.8	393	7	US-11-196-475-114	Sequence 114, App
38	63	6.8	441	7	US-11-196-475-120	Sequence 120, App
39	63	6.8	454	7	US-11-196-475-116	Sequence 116, App
40	63	6.8	588	7	US-11-196-475-122	Sequence 122, App
41	63	6.8	5024	6	US-10-793-626-2964	Sequence 2964, Ap
42	62.5	6.8	3144	7	US-11-055-035-1	Sequence 1, App
43	62	6.7	438	7	US-11-069-642-57	Sequence 57, App
44	62	6.7	450	6	US-10-763-712A-76	Sequence 76, App
45	62	6.7	670	6	US-10-995-561-528	Sequence 528, App

## ALIGNMENTS

RESULT 1  
US-10-522-883-4  
; Sequence 4, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:  
; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131M0  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: r-hil-7 CDNA  
US-10-522-883-4

Query Match 100.0%; Score 922; DB 6; Length 177;  
Best Local Similarity 100.0%; Pred. No. 9.8e-91;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRYIFGHPPLILVLLPVASSDCDIEGKQYSESVLWVSIDQLDSMKETGSNCL 60  
DB 1 MFHVSFRYIFGHPPLILVLLPVASSDCDIEGKQYSESVLWVSIDQLDSMKETGSNCL 60  
QY 61 NNEFNFPEKHICIDANKEGFLFRAARKLRFQIKMNSTGDFDLHLKVSFGTITLLNCTGQ 120  
DB 61 NNEFNFPEKHICIDANKEGFLFRAARKLRFQIKMNSTGDFDLHLKVSFGTITLLNCTGQ 120  
QY 121 VGRKPPALGEQPTKSLPEKNSLKEKKLNDLCPKRLLOIKTCWNKILMGTEKH 177  
DB 121 VGRKPPALGEQPTKSLPEKNSLKEKKLNDLCPKRLLOIKTCWNKILMGTEKH 177  
RESULT 2  
US-10-522-883-13  
; Sequence 13, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:  
; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131M0  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02  
; NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.1  
; SEQ ID NO 13  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PS-sil-7 CDNA  
US-10-522-883-13

Query Match 97.1%; Score 895; DB 6; Length 177;  
Best Local Similarity 96.6%; Pred. No. 7.1e-88;  
Matches 171; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFHVSFRITFGLPPLILVLFPVASSDCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCL 60  
DB 1 MFHVSFRITFGLPPLILVLFPVASSDCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCL 60  
QY 61 NNEFNFFKRRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFNFFKRRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGK 120  
QY 121 VKGRKPAALGEPQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VKGRKPAALGEPQPTKSLSEENKSLKEQKKLNDSCFLKRLLOEIKTCWNKILMGTEKH 177

## RESULT 3

US-10-522-883-19  
; Sequence 19, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:  
; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 19  
; LENGTH: 173  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: HMM38PS-r-hil-7 CDNA  
US-10-522-883-19

Query Match 88.4%; Score 815; DB 6; Length 173;  
Best Local Similarity 95.7%; Pred. No. 2e-79;  
Matches 156; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 15 LILVLLPVASSDCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCLNNEFNFFKRRHICDA 74  
DB 11 LILVLLPVASSDCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCLNNEFNFFKRRHICDA 70  
QY 75 NKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALGEP 134  
DB 71 NKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALGEP 130  
QY 135 TKSLEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 131 TKSLEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 173

## RESULT 4

US-10-522-883-17  
; Sequence 17, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:  
; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02

NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 17  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: EPOPS-r-hil-7 CDNA  
US-10-522-883-17

Query Match 86.8%; Score 800.5; DB 6; Length 179;  
Best Local Similarity 93.4%; Pred. No. 7.2e-76;  
Matches 156; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

QY 11 GLPPLILVLFPVASSDCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCLNNEFNFFKRRH 70  
DB 22 GLPPL-----GDDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCLNNEFNFFKRRH 72  
QY 71 ICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALG 130  
DB 73 ICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALG 132  
QY 131 EAQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 133 EAQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTEKH 179

## RESULT 5

US-10-522-883-2  
; Sequence 2, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:  
; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: r-hil-7 CDNA  
US-10-522-883-2

Query Match 86.3%; Score 796; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 1.8e-77;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCLNNEFNFFKRRHICDANKEGMFLFRAA 85  
DB 2 DCDIEGDKGQYESVLMVSIIDQLDSMKEIGSNCLNNEFNFFKRRHICDANKEGMFLFRAA 61  
QY 86 RKLQFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALGEPQPTKSLSEENKSLK 145  
DB 62 RKLQFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALGEPQPTKSLSEENKSLK 121  
QY 146 EOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 122 EOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 153

## RESULT 6

US-10-522-883-23  
; Sequence 23, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:  
; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883

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; CURRENT FILING DATE: 2005-02-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: HMM38PS-sil-7
US-10-522-883-23

```

```

Query Match      85.5%; Score 788; DB 6; Length 173;
Best Local Similarity 92.0%; Pred. No. 1.5e-76;
Matches 150; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

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QY 15 LILVILPVASSDDIEGKQKQYESVLMWSIDQLDLSMKEIGSNCINNEFPKRLHCDA 74
DB 11 LILVILPVWADCDIEGKQKQYESVLMWSIDQLDLSMKEIGSNCINNEFPKRLHCDD 70
QY 75 NKEGMFLPFAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGVKGRKPAALGEAOP 134
DB 71 NKEGMFLPFAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGVKGRKPAALGEPOP 130
QY 135 TKSLEENKSLKEQKQKINDLCFLKRLLOEIKTKCNKILMGTKKH 177
DB 131 TKSLEENKSLKEQKQKINDSCFLKRLLOEIKTKCNKILMGTKKH 173

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RESULT 7
US-10-522-883-21
; Sequence 21, Application US/10522883
; Publication No. US20050249701A1
; GENERAL INFORMATION:
; APPLICANT: CYTHERIS
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
; FILE REFERENCE: B013IWO
; CURRENT APPLICATION NUMBER: US/10/522,883
; CURRENT FILING DATE: 2005-02-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: EPOPS-sil-7 cDNA
US-10-522-883-21

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Query Match
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```

Best Local Similarity 89.8%; Pred. No. 5.2e-75;
Matches 150; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

```

```

QY 11 GLPPLILVLPVASSDDIEGKQKQYESVLMWSIDQLDLSMKEIGSNCINNEFPKKH 70
DB 22 GLPVL-----GDCDIEGKQKQYESVLMWSIDQLDLSMKEIGSNCINNEFPKKH 72
QY 71 ICDANEGMFLPFAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGVKGRKPAALG 130
DB 73 LCDNNEGMFLPFAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGVKGRKPAALG 132
QY 131 EAQPTKSLEENKSLKEQKQKINDLCFLKRLLOEIKTKCNKILMGTKKH 177
DB 133 EQPTKSLEENKSLKEQKQKINDSCFLKRLLOEIKTKCNKILMGTKKH 179

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```

RESULT 8
US-11-191-374-18
; Sequence 18, Application US/11191374
; Publication No. US20050260673A1
; GENERAL INFORMATION:
; APPLICANT: Hresko, Michelle Coucu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Williams, Deryck J.

```

```

; APPLICANT: Frevert, Anita M.
; APPLICANT: Chiappelli, Brandi
; APPLICANT: Baulite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Bradley, John D.
; APPLICANT: Xu, Siqun
; TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
; FILE REFERENCE: 12557-015001
; CURRENT APPLICATION NUMBER: US/11/191,374
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/771,708
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/444,771
; PRIOR FILING DATE: 2003-02-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-191-374-18

```

```

Query Match      8.4%; Score 77.5; DB 7; Length 741;
Best Local Similarity 25.5%; Pred. No. 1.6;
Matches 35; Conservative 16; Mismatches 35; Indels 51; Gaps 7;

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```

QY 13 PPLILVLPVASSDDIEGKQKQYESVLMWSIDQLDLSMKEIGSNCINNEFPKRLHC 72
DB 435 PP-----PTVSSDCGTVIRDKM-EALVWSLDGVLPHQ-----VTEWDFRFRSC 480
QY 73 DAN-----KEGMF-----LFAARKLRQFLKMNSTGDPDLHLKVSSEGTILLNCTGVKG 123
DB 481 DVSMDKMKVKGSSVVTITVEAS-----SQNTTVLDVAT----- 513
QY 124 RKPALGEAOPKSLKEE 140
DB 514 -PPVSABQLINQLEE 529

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```
RESULT 9
US-11-191-375-18
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; Sequence 18, Application US/11191375
; Publication No. US20050260674A1
; GENERAL INFORMATION:
; APPLICANT: Hresko, Michelle Coucu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Williams, Deryck J.
; APPLICANT: Frevert, Anita M.
; APPLICANT: Chiappelli, Brandi
; APPLICANT: Baulite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Bradley, John D.
; APPLICANT: Xu, Siqun
; TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
; FILE REFERENCE: 12557-015001
; CURRENT APPLICATION NUMBER: US/11/191,375
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/771,708
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/444,771
; PRIOR FILING DATE: 2003-02-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-191-375-18

```

```
Query Match      8.4%; Score 77.5; DB 7; Length 741;
Best Local Similarity 25.5%; Pred. No. 1.6;
Matches 35; Conservative 16; Mismatches 35; Indels 51; Gaps 7;

QY 13 PPLILVLPVASSDCDIEGKGYESVLMVSIQDLDSMKEISNCLNNEFFFKRHIC 72
DB 435 PP-----PVTSSDCGTVIRDKM-EALVVVSLDGVLPHQ-----VTTWDRFYRVSC 480
QY 73 DAN-----KEGMF-----LFRARKLRQFLKNNSTGDPDLHLKXSEGTITLNCYGQVG 123
DB 481 DVSDMKVAKESGVVTTIYRAS-----SQTITVDVAT----- 513
QY 124 RKPAALGEAOPTKSLEE 140
DB 514 -PPVSAELQILNQLEE 529

RESULT 10
US-11-191-588-18
; Sequence 18, Application US/11191588
; Publication No. US20050282222A1
; GENERAL INFORMATION:
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaidd, Merry B.
; APPLICANT: Williams, Deryck J.
; APPLICANT: Frevert, Anita M.
; APPLICANT: Chapelli, Brandi
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Bradley, John D.
; APPLICANT: Xu, Siqun
; TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
; FILE REFERENCE: 12557-015001
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/11/191,588
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/444,771
; PRIOR FILING DATE: 2003-02-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-191-588-18

Query Match      8.4%; Score 77.5; DB 7; Length 741;
Best Local Similarity 25.5%; Pred. No. 1.6;
Matches 35; Conservative 16; Mismatches 35; Indels 51; Gaps 7;

QY 13 PPLILVLPVASSDCDIEGKGYESVLMVSIQDLDSMKEISNCLNNEFFFKRHIC 72
DB 435 PP-----PVTSSDCGTVIRDKM-EALVVVSLDGVLPHQ-----VTTWDRFYRVSC 480
QY 73 DAN-----KEGMF-----LFRARKLRQFLKNNSTGDPDLHLKXSEGTITLNCYGQVG 123
DB 481 DVSDMKVAKESGVVTTIYRAS-----SQTITVDVAT----- 513
QY 124 RKPAALGEAOPTKSLEE 140
DB 514 -PPVSAELQILNQLEE 529

RESULT 11
US-11-191-374-46
; Sequence 46, Application US/11191374
; Publication No. US20050260673A1
; GENERAL INFORMATION:
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaidd, Merry B.
```

```
; APPLICANT: Williams, Deryck J.
; APPLICANT: Frevert, Anita M.
; APPLICANT: Chapelli, Brandi
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Bradley, John D.
; APPLICANT: Xu, Siqun
; TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
; FILE REFERENCE: 12557-015001
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/771,708
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/444,771
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Caenorhabditis briggsae
US-11-191-374-46

Query Match      8.2%; Score 75.5; DB 7; Length 742;
Best Local Similarity 24.8%; Pred. No. 2.6;
Matches 34; Conservative 17; Mismatches 35; Indels 51; Gaps 7;

QY 13 PPLILVLPVASSDCDIEGKGYESVLMVSIQDLDSMKEISNCLNNEFFFKRHIC 72
DB 436 PP-----PVTSSDCGTVIRDKM-EALVVVSLDGVLPHQ-----VTTWDRFYRVSC 481
QY 73 DAN-----KEGMF-----LFRARKLRQFLKNNSTGDPDLHLKXSEGTITLNCYGQVG 123
DB 482 DVSDMKVAKESGVVTTIYRAS-----SQTITVDVAT----- 514
QY 124 RKPAALGEAOPTKSLEE 140
DB 515 -PPVTAELQILNQLEE 530

RESULT 12
US-11-191-375-46
; Sequence 46, Application US/11191375
; Publication No. US20050260674A1
; GENERAL INFORMATION:
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaidd, Merry B.
; APPLICANT: Williams, Deryck J.
; APPLICANT: Frevert, Anita M.
; APPLICANT: Chapelli, Brandi
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Bradley, John D.
; APPLICANT: Xu, Siqun
; TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
; FILE REFERENCE: 12557-015001
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/771,708
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/444,771
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Caenorhabditis briggsae
US-11-191-375-46
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Query Match 7.9%; Score 72.5; DB 7; Length 291;  
 Best Local Similarity 24.8%; Pred. No. 1.6;  
 Matches 35; Conservative 21; Mismatches 48; Indels 37; Gaps 6.

QY 26 DCQIE-GKDGQYEVLMVSIIDQLLSMKELGSCILNN-EPNFKRHICDANKSGMFLER 83  
 176 DCYVENGLISVLDLGLVMTTIISSKCDKGEVNVQTVTELKNTLTGRELCPAVKEDVDLFL 234

QY 84 AARKLROFLKMNSTGDPDIHLKVS-----EGTTLINCTGQVGRKPPALGEAOP 134  
Db 235 -----LTGTPDEYVEQVAQYKALPVLJENARILNVCV-----DAXM 270  
QY 135 TKSLEENK-SLKEOKKLDLC 154  
Db 271 TEEDKENALSLDKIYTSPLC 291

Search completed: December 29, 2005, 14:35:42  
Job time : 15 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 14:13:45 ; Search time 48 Seconds  
(without alignments)  
304.867 Million cell updates/sec

Title: US-10-706-801-1

Perfect score: 922  
Sequence: 1 MHVSVFRYIFGPPILVL.....RLQEIKTCKNKLMTKEH 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 segs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5.COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6.COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H.COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS.COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE.COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/BACKLIST1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	922	100.0	177	1	US-08-284-393B-7
2	922	100.0	177	1	US-08-446-908-4
3	922	100.0	177	1	US-08-231-205A-4
4	922	100.0	177	1	US-08-871-161-4
5	922	100.0	177	2	US-09-462-941-14
6	922	100.0	177	4	PCT-US95-08950-7
7	922	100.0	200	2	US-09-949-016-8732
8	796	86.3	152	1	US-08-318-193-84
9	765.5	83.0	151	6	5229115-1
10	536.5	58.2	154	1	US-08-446-908-2
11	536.5	58.2	154	1	US-08-231-205A-2
12	536.5	58.2	154	1	US-08-871-161-2
13	425	46.1	89	2	US-09-621-976-6992
14	409.5	44.4	129	6	5229115-2
15	140.5	15.2	280	1	US-08-249-189-23
16	140.5	15.2	280	1	US-08-484-624A-23
17	140.5	15.2	280	1	US-08-477-733B-23
18	140.5	15.2	280	2	US-09-088-913A-23
19	140.5	15.2	280	2	US-08-769-819-23
20	140.5	15.2	280	2	US-08-770-974-23
21	140.5	15.2	280	2	US-08-770-981-23
22	137.5	14.9	216	1	US-08-106-507-10
23	137.5	14.9	216	1	US-08-446-922-8
24	137.5	14.9	216	4	PCT-US93-10034-8
25	136.5	14.8	273	1	US-08-446-922-11
26	136.5	14.8	273	1	US-08-249-189-21
27	136.5	14.8	273	1	US-08-249-189-21

28	136.5	14.8	273	1	US-08-484-624A-21	Sequence 21, App1
29	136.5	14.8	273	1	US-08-477-733B-21	Sequence 21, App1
30	136.5	14.8	273	2	US-08-088-913A-21	Sequence 21, App1
31	136.5	14.8	273	2	US-08-769-819-21	Sequence 21, App1
32	136.5	14.8	273	2	US-08-770-974-21	Sequence 21, App1
33	136.5	14.8	273	2	US-08-770-981-21	Sequence 21, App1
34	136.5	14.8	273	2	US-09-399-106-21	Sequence 21, App1
35	134.5	14.6	158	2	US-08-620-694A-7	Sequence 7, App1
36	134.5	14.6	158	2	US-09-022-255-7	Sequence 7, App1
37	134.5	14.6	158	2	US-09-022-259-7	Sequence 7, App1
38	134.5	14.6	158	2	US-09-022-263-7	Sequence 7, App1
39	134.5	14.6	158	2	US-09-022-267-7	Sequence 7, App1
40	134.5	14.6	158	2	US-09-022-257-7	Sequence 7, App1
41	134.5	14.6	158	2	US-09-022-257-7	Sequence 7, App1
42	134.5	14.6	158	2	US-09-549-679-7	Sequence 7, App1
43	126.5	13.7	473	1	US-08-249-189-16	Sequence 16, App1
44	126.5	13.7	473	1	US-08-484-624A-16	Sequence 16, App1
45	126.5	13.7	473	1	US-08-477-733B-16	Sequence 16, App1

#### ALIGNMENTS

RESULT 1  
US-08-284-393B-7  
; Sequence 7, Application US/08284393B  
; Patent No. 5696234  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: DNA Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/284,393B  
; FILING DATE: 01-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0389  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-284-393B-7

Query Match 100.0%; Score 922; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-101;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVSVFRYIFGPPILVLVLPVASSDCDIEGDKGYEVSILAWVSIDQLDSMKETGSNCL 60  
DB 1 MHVSVFRYIFGPPILVLVLPVASSDCDIEGDKGYEVSILAWVSIDQLDSMKETGSNCL 60  
QY 61 NNEFNFPRKHICDANKGMFLFRAARKLQRQILKNSTGDFDLHLKLVSEGTTLINCTGQ 120

Db 61 NNEFNFFRRHICDANKGEMFLFRARKLRQFLKNNSTGDPDLHLKVSSEGTILLNCTGQ 120  
Qy 121 VKGRKPAALGEAOPKTSLEENKSLKEOKKNDLCFLKRLQEIKTCKNKLIMGTKEH 177  
Db 121 VKGRKPAALGEAOPKTSLEENKSLKEOKKNDLCFLKRLQEIKTCKNKLIMGTKEH 177

## RESULT 2

US-08-446-908-4  
; Sequence 4, Application US/08446908  
; Patent No. 5705149  
; GENERAL INFORMATION:  
; APPLICANT: Namen, Anthony E.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Lupton, Stephen D.  
; APPLICANT: Mochizuki, Diane Y.  
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
; TITLE OF INVENTION: Therewith  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,908  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/231,205  
; FILING DATE: 21-APR-1994  
; APPLICATION NUMBER: US 07/957,649  
; FILING DATE: 06-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,438  
; FILING DATE: 13-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/255,209  
; FILING DATE: 07-OCT-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/113,566  
; FILING DATE: 26-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2104-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-446-908-4

Query Match 100.0%; Score 922; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-10; Mismatches 0; Indels 0; Gaps 0;  
Matches 177; Conservative 0;

Qy 1 MFHVSFRITFGPLPLIIVLVPVASSDCDIEGKDGKQYESVLMVSIIDQLDSMKEIGSNCL 60  
Db 1 MFHVSFRITFGPLPLIIVLVPVASSDCDIEGKDGKQYESVLMVSIIDQLDSMKEIGSNCL 60

Qy 61 NNEFNFFRRHICDANKGEMFLFRARKLRQFLKNNSTGDPDLHLKVSSEGTILLNCTGQ 120  
Db 61 NNEFNFFRRHICDANKGEMFLFRARKLRQFLKNNSTGDPDLHLKVSSEGTILLNCTGQ 120  
Qy 121 VKGRKPAALGEAOPKTSLEENKSLKEOKKNDLCFLKRLQEIKTCKNKLIMGTKEH 177  
Db 121 VKGRKPAALGEAOPKTSLEENKSLKEOKKNDLCFLKRLQEIKTCKNKLIMGTKEH 177

## RESULT 3

US-08-231-205A-4  
; Sequence 4, Application US/08231205A  
; Patent No. 5714585  
; GENERAL INFORMATION:  
; APPLICANT: Namen, Anthony E.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Lupton, Stephen D.  
; APPLICANT: Mochizuki, Diane Y.  
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
; TITLE OF INVENTION: Therewith  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/231,205A  
; FILING DATE: 21-APR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/957,649  
; FILING DATE: 06-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,438  
; FILING DATE: 13-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/255,209  
; FILING DATE: 07-OCT-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/113,566  
; FILING DATE: 26-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2104-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-231-205A-4

Query Match 100.0%; Score 922; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-10; Mismatches 0; Indels 0; Gaps 0;  
Matches 177; Conservative 0;

Qy 1 MFHVSFRITFGPLPLIIVLVPVASSDCDIEGKDGKQYESVLMVSIIDQLDSMKEIGSNCL 60  
Db 1 MFHVSFRITFGPLPLIIVLVPVASSDCDIEGKDGKQYESVLMVSIIDQLDSMKEIGSNCL 60  
Qy 61 NNEFNFFRRHICDANKGEMFLFRARKLRQFLKNNSTGDPDLHLKVSSEGTILLNCTGQ 120



Db 61 NNEFNFFKRIHICDANKGEMFLFRARKLRQPLKXNSTGDFDHLKLVSEGTILLNCTGQ 120  
QY 121 VKGRPALGEAOPTKSLEENKSLKEOKKANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
Db 121 VKGRPALGEAOPTKSLEENKSLKEOKKANDLCLFKRLLOEIKTCWNKILMGTEKH 177

## RESULT 4

US-08-871-161-4  
; Sequence 4, Application US/08871161  
; Patent No. 5965122  
; GENERAL INFORMATION:  
; APPLICANT: Namen, Anthony E.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Lupton, Stephen D.  
; APPLICANT: Mochizuki, Diane Y.  
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
; TITLE OF INVENTION: Therewith  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,161  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,908  
; FILING DATE: 22-MAY-1995  
; APPLICATION NUMBER: US 08/231,205  
; FILING DATE: 21-APR-1994  
; APPLICATION NUMBER: US 07/957,649  
; FILING DATE: 06-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,438  
; FILING DATE: 13-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/255,209  
; FILING DATE: 07-OCT-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/113,566  
; FILING DATE: 26-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2104-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-871-161-4

QY 1 MFHVSFRYIFGIPLLIVLVPVASSDCDIEGKGQYSESVLWMSIDQLDSMKEIGSNCL 60  
Query Match 100.0%; Score 922; DB 1; Length 177;  
Best local similarity 100.0%; Pred. No. 3.8e-101; Indels 0; Gaps 0;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MFHVSFRYIFGIPLLIVLVPVASSDCDIEGKGQYSESVLWMSIDQLDSMKEIGSNCL 60  
QY 61 NNEFNFFKRIHICDANKGEMFLFRARKLRQPLKXNSTGDFDHLKLVSEGTILLNCTGQ 120  
Db 61 NNEFNFFKRIHICDANKGEMFLFRARKLRQPLKXNSTGDFDHLKLVSEGTILLNCTGQ 120  
QY 121 VKGRPALGEAOPTKSLEENKSLKEOKKANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
Db 121 VKGRPALGEAOPTKSLEENKSLKEOKKANDLCLFKRLLOEIKTCWNKILMGTEKH 177

## RESULT 5

US-09-462-941-14  
; Sequence 14, Application US/09462941  
; Patent No. 6608183  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N.  
; APPLICANT: Bolder Biotechnology, Inc.  
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins  
; FILE REFERENCE: 4152-1-PUS  
; CURRENT APPLICATION NUMBER: US/09/462,941  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/052,516  
; PRIOR FILING DATE: 1997-07-14  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-462-941-14

Query Match 100.0%; Score 922; DB 2; Length 177;  
Best local similarity 100.0%; Pred. No. 3.8e-101; Indels 0; Gaps 0;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRYIFGIPLLIVLVPVASSDCDIEGKGQYSESVLWMSIDQLDSMKEIGSNCL 60  
Db 1 MFHVSFRYIFGIPLLIVLVPVASSDCDIEGKGQYSESVLWMSIDQLDSMKEIGSNCL 60  
QY 61 NNEFNFFKRIHICDANKGEMFLFRARKLRQPLKXNSTGDFDHLKLVSEGTILLNCTGQ 120  
Db 61 NNEFNFFKRIHICDANKGEMFLFRARKLRQPLKXNSTGDFDHLKLVSEGTILLNCTGQ 120  
QY 121 VKGRPALGEAOPTKSLEENKSLKEOKKANDLCLFKRLLOEIKTCWNKILMGTEKH 177  
Db 121 VKGRPALGEAOPTKSLEENKSLKEOKKANDLCLFKRLLOEIKTCWNKILMGTEKH 177

## RESULT 6

PCT-US95-08950-7  
; Sequence 7, Application PCT/TUS9508950  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/08950  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/284,393  
FILING DATE: 01-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08950-7

Query Match 100.0%; Score 922; DB 4; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3,8e-101;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRITFGIPPLILVLPVASSDCIEGKQGYESVLMVSIIDQLDSMKEIGSNCL 60  
DB 1 MFHVSFRITFGIPPLILVLPVASSDCIEGKQGYESVLMVSIIDQLDSMKEIGSNCL 60  
QY 61 NNEFFFRKHICDANKGKGFLEFRARKLROFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 61 NNEFFFRKHICDANKGKGFLEFRARKLROFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
QY 121 VKGRKPAALGEAOPTKSLSEENKSLKEOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 121 VKGRKPAALGEAOPTKSLSEENKSLKEOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 177

RESULT 7  
US-09-949-016-8732  
Sequence 8732, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8732  
LENGTH: 200  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8732

Query Match 100.0%; Score 922; DB 2; Length 200;  
Best Local Similarity 100.0%; Pred. No. 4,5e-101;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHVSFRITFGIPPLILVLPVASSDCIEGKQGYESVLMVSIIDQLDSMKEIGSNCL 60  
DB 24 MFHVSFRITFGIPPLILVLPVASSDCIEGKQGYESVLMVSIIDQLDSMKEIGSNCL 83  
QY 61 NNEFFFRKHICDANKGKGFLEFRARKLROFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 120  
DB 84 NNEFFFRKHICDANKGKGFLEFRARKLROFLKMNSTGDFDLHLKVSSEGTILLNCTGQ 143

QY 121 VKGRKPAALGEAOPTKSLSEENKSLKEOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 144 VKGRKPAALGEAOPTKSLSEENKSLKEOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 200

RESULT 8  
US-08-318-193-84  
Sequence 84, Application US/08318193  
Patent No. 5641663  
GENERAL INFORMATION:  
APPLICANT: GARVIN, Robert T.  
APPLICANT: MALEK, Lawrence T.  
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION  
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY  
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS  
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,193  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,314  
FILING DATE:  
APPLICATION NUMBER: US 07/224,568  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/116 CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 152 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-193-84

Query Match 86.3%; Score 796; DB 1; Length 152;  
Best Local Similarity 100.0%; Pred. No. 2,7e-86;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DCDIEGKQGYESVLMVSIIDQLDSMKEIGSNCLNNEFFFRKHICDANKGKGFLEFRAA 85  
DB 1 DCDIEGKQGYESVLMVSIIDQLDSMKEIGSNCLNNEFFFRKHICDANKGKGFLEFRAA 60  
QY 86 RKLROFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALGEAOPTKSLSEENKSLK 145  
DB 61 RKLROFLKMNSTGDFDLHLKVSSEGTILLNCTGQVGRKPAALGEAOPTKSLSEENKSLK 120  
QY 146 EOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 177  
DB 121 EOKKLNDCFLKRLLOEIKTCWNKILMGTEKH 152

RESULT 9  
5229115-1  
Patent No. 5229115

APPLICANT: LYNCH, DAVID H.  
TITLE OF INVENTION: ADOPTIVE IMMUNOTHERAPY WITH INTERLEUKIN-7  
NUMBER OF SEQUENCES: 2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/559,001  
FILING DATE: 26-JUL-1990  
SEQ ID NO: 1:  
LENGTH: 151  
5229115-1

Query Match 83.0%; Score 765.5; DB 6; Length 151;  
Best Local Similarity 98.0%; Pred. No. 1.1e-82;  
Matches 149; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 26 DCDIEGKDKQYVESVLMVSIIDLLDSMKEIGSNCLNNEFNFKRHICDANKEGMFLFRAA 85  
DB 1 DCDIGKDKQYVESVLMVSIIDLLDSMKEIGSNCLNNEFNFKRHICDANKEGMFLFRAA 60  
QY 86 RKLROPLKRNSTGDFPLHLKVSSEGTTLINCTGVKGRKPAALGSAOPTKSLSEENKSLK 145  
DB 61 RKLROPLKRNSTGDFPLHLKVSSEGTTLINCTGVKGRKPAALGSAOPTKSL-ENKSLK 119  
QY 146 EOKKNDLCLFKRLLOEIKTCWNKILMGTEH 177  
DB 120 EOKKNDLCLFKRLLOEIKTCWNKILMGTEH 151

## RESULT 10

US-08-446-908-2  
Sequence 2, Application US/08446908  
Patent No. 5705149  
GENERAL INFORMATION:  
APPLICANT: Namen, Anthony E.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Lupton, Stephen D.  
APPLICANT: Mochizuki, Diane Y.  
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,908  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,205  
FILING DATE: 21-APR-1994  
APPLICATION NUMBER: US 07/957,649  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,438  
FILING DATE: 13-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/255,209  
FILING DATE: 07-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,566  
FILING DATE: 26-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2104-D

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-908-2

Query Match 58.2%; Score 536.5; DB 1; Length 154;  
Best Local Similarity 61.5%; Pred. No. 1.7e-55;  
Matches 107; Conservative 21; Mismatches 25; Indels 21; Gaps 3;

QY 1 MFHVSFRYIFGILPILVTLPPVASSDCDIEGDKQYVESVLMVSIIDLLDSMKEIGSNCL 60  
DB 1 MFHVSFRYIFGILPILVTLPPVASSDCDIEGDKQYVESVLMVSIIDLLDSMKEIGSNCL 59  
QY 61 NNEFNFKRHICDANKEGMFLFRAARKLROPLKRNSTGDFPLHLKVSSEGTTLINCTGV 120  
DB 60 NNEFNFKRHICDANKEGMFLFRAARKLROPLKRNSTGDFPLHLKVSSEGTTLINCTGV 118  
QY 121 VKGRKPAALGSAOPTKSLSEENKSLK EOKKNDLCLFKRLLOEIKTCWNKILMGTEH 174  
DB 119 VKGRKPAALGSAOPTKSLSEENKSLK EOKKNDLCLFKRLLOEIKTCWNKILMGTEH 153

## RESULT 11

US-08-231-205A-2  
Sequence 2, Application US/08231205A  
Patent No. 5714585  
GENERAL INFORMATION:  
APPLICANT: Namen, Anthony E.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Lupton, Stephen D.  
APPLICANT: Mochizuki, Diane Y.  
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,205A  
FILING DATE: 21-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/957,649  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,438  
FILING DATE: 13-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/255,209  
FILING DATE: 07-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,566  
FILING DATE: 26-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2104-D  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-231-205A-2

Query Match 58.2%; Score 536.5; DB 1; Length 154;  
Best Local Similarity 61.5%; Pred. No. 1.7e-55;  
Matches 107; Conservative 21; Mismatches 25; Indels 21; Gaps 3;

QY 1 MFHVSFRYIFGLPPLILVLPVASSDCDIEGDKQYVESVLMVSIIDQLLSMKEIGSNCL 60  
DB 1 MFHVSFRYIFGLPPLILVLPVTSSECHIKDKEGKAYESVLMISIDE-LDKMTGDSNCP 59  
QY 61 NNEFNPFKRHICDANKEGMFLFRAARKLRQFLKKNSTGDPDLHLKYSBGTTLINCTGQ 120  
DB 60 NNEFNPFKRHVCDPTKEAFLNRAARKLRQFLKKNISSEFVHLTLTVSOGTTLVNCTG 118  
QY 121 VKGRPALGEAQPITKSLSEENKSLKEOKKNDLCFLKRLLOEIKTCNNKILMGT 174  
DB 119 -----KEEKVKEQKK-NDACFLKRLRLREIKTCNNKILKGS 153

RESULT 12

US-08-871-161-2  
Sequence 2, Application US/08871161  
Patent No. 5965122

GENERAL INFORMATION:  
APPLICANT: Namen, Anthony E.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Lupion, Stephen D.  
APPLICANT: Mochizuki, Diane Y.  
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
TITLE OF INVENTION: Therewith  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,161  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,908  
FILING DATE: 22-MAY-1995  
APPLICATION NUMBER: US 08/231,205  
FILING DATE: 21-APR-1994  
APPLICATION NUMBER: US 07/957,649  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,438  
FILING DATE: 13-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/255,209  
FILING DATE: 07-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,566  
FILING DATE: 26-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2104-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-161-2

Query Match 58.2%; Score 536.5; DB 1; Length 154;  
Best Local Similarity 61.5%; Pred. No. 1.7e-55;  
Matches 107; Conservative 21; Mismatches 25; Indels 21; Gaps 3;

QY 1 MFHVSFRYIFGLPPLILVLPVASSDCDIEGDKQYVESVLMVSIIDQLLSMKEIGSNCL 60  
DB 1 MFHVSFRYIFGLPPLILVLPVTSSECHIKDKEGKAYESVLMISIDE-LDKMTGDSNCP 59  
QY 61 NNEFNPFKRHICDANKEGMFLFRAARKLRQFLKKNSTGDPDLHLKYSBGTTLINCTGQ 120  
DB 60 NNEFNPFKRHVCDPTKEAFLNRAARKLRQFLKKNISSEFVHLTLTVSOGTTLVNCTG 118  
QY 121 VKGRPALGEAQPITKSLSEENKSLKEOKKNDLCFLKRLLOEIKTCNNKILMGT 174  
DB 119 -----KEEKVKEQKK-NDACFLKRLRLREIKTCNNKILKGS 153

RESULT 13

US-09-621-976-6902  
Sequence 6902, Application US/09621976  
Patent No. 6639063

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET 054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 6902  
LENGTH: 89  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-621-976-6902

Query Match 46.1%; Score 425; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 MKEIGSNCLNNEFNPFKRHICDANKEGMFLFRAARKLRQFLKKNSTGDPDLHLKYSBGT 111  
DB 1 MKEIGSNCLNNEFNPFKRHICDANKEGMFLFRAARKLRQFLKKNSTGDPDLHLKYSBGT 60  
QY 112 TILNCTGVKGRKRALGEA 132  
DB 61 TILNCTGVKGRKRALGEA 81

RESULT 14

5229115-2  
Patent No. 5229115  
APPLICANT: LYNCH, DAVID H.  
TITLE OF INVENTION: ADOPTIVE IMMUNOTHERAPY WITH INTERLEUKIN-7  
NUMBER OF SEQUENCES: 2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/559,001  
FILING DATE: 26-JUL-1990  
SEQ ID NO: 2;



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RESULT 6
S03171
Interleukin-7 precursor - mouse
N:Alternate names: IL-7
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S03171; B43527
R:Name: A.E.; Lupcon, S.; Hjertild, K.; Wignall, J.; Mochizuki, D.Y.; Schmler, A.; Mc
Nature 333, 571-573, 1988
A>Title: Stimulation of B-cell progenitors by cloned murine interleukin-7.
A:Reference number: S03171; MUID:88232938; PMID:3259677
A:Accession: S03171
A:Molecule type: mRNA
A:Residues: 1-154 <NMA>
A:Cross-references: UNIPROT:P10168; UNIPARC:UPI000004032; EMBL:X07962; NID:952694; PIDN
A>Note: part of this sequence, including the amino end of the mature protein, was confir
R:Lupcon, S.D.; Gimpel, S.; Jerez, R.; Bruntton, L.L.; Hjertild, K.A.; Coeman, D.; Goodwi
J. Immunol. 144, 3592-3601, 1990
A>Title: Characterization of the human and murine IL-7 genes.
A:Reference number: A43527; MUID:90229755; PMID:2329282
A:Accession: B43527
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-119 <LUP>
A:Cross-references: UNIPARC:UPI000017673F; GB:M29054
C:Superfamily: Interleukin-7
C:Keywords: cytokine; growth factor
F:1-25/Domain: signal sequence #status predicted <STM>
F:26-154/Product: Interleukin-7 #status predicted <MAT>

Query Match          58.2%; Score 536.5; DB 2; Length 154;
Best Local Similarity 61.5%; Pred. No. 3.4e-41;
Matches 107; Conservative 21; Mismatches 25; Indels 21; Gaps 3;

QY 1 MEHVSFRYIFGLPPLIVLLPVASSDCDIEGDKQYSEVLMVSIIDQLDSMKETGSNCL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MEHVSFRYIFGLPPLIVLLPVASSDCDIEGDKQYSEVLMVSIIDQLDSMKETGSNCP 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NNEFNPFRKHIDCANKEGWFELFPAARKLQPLKMNSTGPDFLHLKVSSEGTIILNCTGQ 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 60 NNEFNPFRKHIDCANKEGWFELFPAARKLQPLKMNSTGPDFLHLKVSSEGTIILNCTG 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 VGRKPAALGEAQPSTKLEENKSLKEOKLNDLCEFLKRLLOEIKTCWNKILMG 174
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 119 -----KEEKVKEQKK-NDACFLKRLRLKIKTCWNKILMG 153
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
S40459
ribosomal protein S3 - Chlamydomonas humicola chloroplast (fragment)
C:Species: chloroplast Chlamydomonas humicola
C>Date: 19-May-1994 #sequence_revision 23-Feb-1996 #text_change 10-May-1996
C:Accession: S40459
R:Lin, X.Q.; Huang, C.; Xu, H.
FEBS Lett. 336, 225-230, 1993
A>Title: The unusual rps3-like of f712 is functionally essential and structurally conserv
A:Reference number: S40457; MUID:94085610; PMID:8262234
A:Accession: S40459
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-682 <LIU>
A:Cross-references: UNIPARC:UPI000017CB3D
C:Genetics:
A:Gene: rps3
A:Genome: chloroplast
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match          10.0%; Score 92.5; DB 2; Length 682;
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 37; Conservative 29; Mismatches 51; Indels 31; Gaps 6;

QY 23 ASSDCDIEGDKQYSEVLMVSIIDQLDSMKETGSNCLNNEF-NPEKRHICDANKEGMFL 81

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DB 433 ALSD-SVNFKSARLTREASNTISTNLLANKNINDECRKIKFEYLKQIVKGRSENIYL 491
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 82 FRAA-----RKTRFPLKMNSTGPDFLHLKVSSEGTIILNCTGQVGRKPAALGEAO 133
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 492 YLATTAEARKDLRLKQPLTKRIASFLFGLNLTQTSBASAI-----OE 533
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 134 PTKSLDENKSLKE--OKKLNDCFLKRL 159
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 534 RLKSVLENSSTKPDPEKTLQDV-FLEQI 560
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 8
D64413
cobalamin biosynthesis protein N homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: D64413
R:Bule, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodok, A.
son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:868087
A:Accession: D64413
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1232 <BU>
A:Cross-references: UNIPROT:O58318; UNIPARC:UPI0000065076; GB:U67534; GB:L77117; NID:915
C:Genetics:
A:Map position: FOR837021-840719
A:Start codon: TTG
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match          9.2%; Score 85; DB 2; Length 1232;
Best Local Similarity 24.2%; Pred. No. 17;
Matches 54; Conservative 29; Mismatches 64; Indels 76; Gaps 13;

QY 1 MEHVSFRYIFGLPPLIVLLPVASSDCDIEGDKQYSEVLMVSIIDQLDSMKETGSNCL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 709 MEHVSFRYIFGLPPLIVLLPVASSDCDIEGDKQYSEVLMVSIIDQLDSMKETGSNCL 757
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NN-ENFNPFRKHICDANK-EGMFLFPAARKLQPLKMNSTGPDFLHLKVSSEGTIILNCT 117
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 758 KEVMQYNF-----DENKIDELKTVKINSKLRADVKTST--IYNLMKVDEE---INA 806
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 118 TGQVKG--RKPAALG-----EAOPTKSLER-----NKSILK 145
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 807 VNALGEGFYIPPRVAGAPTKDINCLPTGRNFYSCNPOEIPTKSAVEMGKKLAEDLIINKYLK 866
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 146 EOKKL-----NDLCLKRLLOEIKTCWNKI 170
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 867 EERGKPEYIIGVIVWGSPTMRTKGGDIDGELTDL-GVKPVMKMK 908
    :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
T15689
hypothetical protein C28G1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Mar-2004
C:Accession: T15689
R:Pavellio, T.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C28G1.
A:Reference number: Z18389
A:Accession: T15689
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1322 <PAV>
A:Cross-references: UNIPARC:UPI000017B7DB; EMBL:U41026; NID:g1086701; PID:g1086702; PIDN
C:Genetics:
A:Gene: C28G1.3

```

A;introns: 25/1; 131/3; 150/1; 166/3; 180/3; 204/2; 235/3; 344/3; 385/2; 436/3; 483/2; 7  
F;810-862/Domain: RING finger homology <RNF>

Query Match 9.1%; Score 84; DB 2; Length 1322;

Best Local Similarity 22.6%; Pred. No. 23; Mismatches 57; Indels 34; Gaps 6;

Matches 35; Conservative 29; Mismatches 57; Indels 34; Gaps 6;

Qy 24 SSDSDIEGDKQKQVSLVMSIDQLDSMKEIGSNCLNNEFFPKRHICDANKEGMFLR 83

Db 913 NTDCDVCK-----LMCRCEFGDHKHKGGLADEVNMUK-----ALKK 954

Qy 84 AARLRLQPLKM--NSTGPFDLHLKVSGETTILLNCTGQVGRKPAALGEAOPTKSLLEN 141

Db 955 SEGSLSKETIDTIEHSLRPFKAENSLSDSNAPMDTINEIKGH-----YDSMRKN 1004

Qy 142 KSLKQKKLNDLCFL--KRLQELKCKMKNILMGTK 175

Db 1005 IDVRQKSIIEELGILAEKQLMENR--NKIYLNTR 1036

#### RESULT 10

566717  
hypothetical protein YOL034w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein O2113

C;Species: Saccharomyces cerevisiae

C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 09-Jul-2004

C;Accession: S66717

R;Hbbid: B; Hattenhorst, U.; Hollenberg, C.P.; Ramezani Rad, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66703

A;Accession: S66717

A;Molecule type: DNA

A;Residues: 1-1093 <HAB>

A;Cross-references: UNIPROT:O08204; UNIPARC:UPI000006AC72; EMBL:Z74776; NID:g1419826; PT

A;Experimental source: strain 8288C

C;Genetics:

A;Gene: MIPS:YOL034w

A;Cross-references: SGD:S0005394

A;Map position: 15L

Query Match 9.1%; Score 83.5; DB 2; Length 1093;

Best Local Similarity 24.1%; Pred. No. 20;

Matches 33; Conservative 25; Mismatches 50; Indels 29; Gaps 5;

Qy 44 SIDQLDSMKEIGSN--CLNNEFFPKRHICDANKEGMFLPRAARKLQPLKMNSTGDFD 101

Db 207 SLDLVLDLRELQSGNEQLQDLDPKAKIYHLRQESDKLRKSVESLNDP--QKKGEIE 264

Qy 102 LH-----LLKVSGETTIL-----LNCCTGQVGRKPAAL-----LGEAOPTK 136

Db 265 LHSQLLPVYKVDHREKLNITYKEEYERAKANLRAILKDKKPFANTKTTLENQVELTEKC 324

Qy 137 SLEENKSLKEOKKLNLDL 153

Db 325 SLKTEFLKAKEKINEI 341

#### RESULT 11

T13031

nucleoporin - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C;Accession: T13031

R;Fuller, M.T.; Kiger, A.A.

submitted to the EMBL Data Library, February 1998

A;Description: Nup32D is an essential Drosophila nucleoporin homologous to vertebrate Nu

A;Reference number: Z17589

A;Accession: T13031

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1349 <RFL>

A;Cross-references: UNIPROT:O62613; UNIPARC:UPI000007FEF9; EMBL:AF051396; NID:g2981203; C;Genetics:

A;Gene: nup32D

A;Cross-references: FlyBase:FBgn0021761

A;Map position: 2L

Query Match 9.1%; Score 83.5; DB 2; Length 1349;

Best Local Similarity 23.2%; Pred. No. 26;

Matches 32; Conservative 25; Mismatches 52; Indels 29; Gaps 5;

Qy 41 LMSIDQLDSMKEIGSNCLNNEFFPKRHICD--ANKEGMFLPRAARKLQPLKMNSTG 98

Db 644 LMYVSRMLHSVWQM--RCVNEQF-----CSNLQSECCALLSDRLSLRSLFVHSHVH 694

Qy 99 D-----FDLHLKVSGETTILLNCTGQVGRKPAALGEAOPTKSLLENKSLKEOKKL 150

Db 695 DISSTRVSPFNHLDNRNYSYTIMWGNT-----LPIPRQVLSBQAQVEETRSL 744

Qy 151 NDLCFLKRLLOEIKTCWN 168

Db 745 SALNLFWHACEVISLWN 762

#### RESULT 12

T13991

nucleoporin 154 - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T13991

R;Gigliotti, S.; Callaini, G.; Andone, S.; Ripabelli, G.M.; Pernas-Alonso, R.; Hofmann

J. Cell Biol. 142, 1195-1207, 1998

A;Title: Nup154, a new Drosophila gene essential for male and female gametogenesis is re

A;Reference number: Z17846; PMID:98402529; PMID:9732281

A;Accession: T13991

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1365 <GIG>

A;Cross-references: UNIPROT:O62536; UNIPARC:UPI000007F4FD; EMBL:Y17111; NID:g3046717; PT

C;Genetics:

A;Gene: Nup154

A;Cross-references: FlyBase:FBgn0021761

Query Match 9.1%; Score 83.5; DB 2; Length 1365;

Best Local Similarity 23.2%; Pred. No. 26;

Matches 32; Conservative 25; Mismatches 52; Indels 29; Gaps 5;

Qy 41 LMSIDQLDSMKEIGSNCLNNEFFPKRHICD--ANKEGMFLPRAARKLQPLKMNSTG 98

Db 660 LMYVSRMLHSVWQM--RCVNEQF-----CSNLQSECCALLSDRLSLRSLFVHSHVH 710

Qy 99 D-----FDLHLKVSGETTILLNCTGQVGRKPAALGEAOPTKSLLENKSLKEOKKL 150

Db 711 DISSTRVSPFNHLDNRNYSYTIMWGNT-----LPIPRQVLSBQAQVEETRSL 760

Qy 151 NDLCFLKRLLOEIKTCWN 168

Db 761 SALNLFWHACEVISLWN 778

#### RESULT 13

T24136

hypothetical protein R10E4.8 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T24136

R;Ainscough, R.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19843

A;Accession: T24136

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-339 <WLL>

A;Cross-references: UNIPROT:Q21908; UNIPARC:UPI000006110A; EMBL:Z50874; PIDN:CAA90771.1;

A;Experimental source: clone R10E4

C:Genetics:  
A:Gene: CESP:R10E4.8  
A:Map position: 3  
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK563.3

Query Match 9.0%; Score 83; DB 2; Length 339;  
Best Local Similarity 28.6%; Pred. No. 6.3;  
Matches 28; Conservative 13; Mismatches 37; Indels 20; Gaps 4;

OY 59 CANNENFFKRRHICDANKGEMFLFRAARKLRQFLKKNSTGDPDLHLTKVSEGTILLNCT 118  
DB 20 CLGHSMERKRNICGAMGGAISTYNAKSFQKFK--NGDPSLEIRI-----CS 66

OY 119 GQVKGKRPALGPAOPTKSLERNK--SLKEOKKLANDLC 154  
DB 67 G-----RPVELNEBDLVKLVEEPRLSLERMEKLECC 99

## RESULT 14

B89848

preprotein translocase subunit [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 05-Oct-2004

C:Accession: B89848  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:11311952; PMID:11418146

A:Accession: B89848

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-843 <KUR>

A:Cross-references: UNIPROT:Q99VM2; UNIPARC:UPI000005226D; GB:BA000018; PTD:G13700644; E

A:Experimental source: strain N315

C:Genetics:

A:Gene: secA

C:Superfamily: preprotein translocase, subunit SecA

Query Match 9.0%; Score 83; DB 2; Length 843;  
Best Local Similarity 24.4%; Pred. No. 17;  
Matches 38; Conservative 22; Mismatches 62; Indels 34; Gaps 7;

OY 28 DIEGDKGYESVLMWSIDQLDSMKIEGSCNNEFFFKR-----HICDANKEG 78  
DB 679 DIKGDAEDIEFVNAKIEAAYOSQKI-----LEEQMEFERMILIRSDISHWT-DHDT 733

OY 79 MFLFPAARKLRQFLKKNSTGDPDLHLTKVSEGT-TILLNCTGQVKG---RK 125  
DB 734 MDQLRGHILRSYAQONPLRDYONEGHELFDIMQNIIEEDTCFKILKSVQVEDNIEREK 793

OY 126 PAALGPAOPTKSLERNKSLK-----EQKLANDLC 154  
DB 794 TTFEGEAKHVSADGKEKVKPKPIYKGDVGRNDG 829

## RESULT 15

H70348

Probable 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) - Aquifex aeolicus  
C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C:Accession: H70348

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; PMID:98196666; PMID:9537320

A:Accession: H70348

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-407 <AQF>

A:Cross-references: UNIPROT:O66820; UNIPARC:UPI00000563AE; GB:AE000695; NID:G2983180; PI

A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: bopC  
C:Superfamily: cofactor-independent phosphoglycerate mutase, archaeal type  
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 8.9%; Score 82.5; DB 2; Length 407;  
Best Local Similarity 24.8%; Pred. No. 8.6;  
Matches 29; Conservative 20; Mismatches 39; Indels 29; Gaps 4;

OY 10 FGLPPLILVLLFVAASDCDIEGDKGYESVLMWSIDQLDSMKIEGSCNNEFFFKR 69  
DB 246 FGKPCICIAVPEPMYKGLASLVGMVDVIEFG---STODEIDITLKVM-----NEYDYFV 297

OY 70 HIC-----DANKGEMFLFRAARKLRQFLKKNSTGDPDLHLTKVSEGTILLNCTG 119  
DB 298 HIKKTDSYGEDGNYEG-----KVSIEDPDHLPQLELKPDLAITG 340

Search completed: December 29, 2005, 14:21:47  
Job time : 45 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2005, 14:10:29 / Search time 230 Seconds

(without alignments)  
542,950 Million cell updates/sec

Title: US-10-706-801-1

Perfect score: 922

Sequence: 1 MEHVSFRYIFGLPPLILVL.....RLLOIKTCWKLNGTKEH 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	922	100.0	177	1 IL7_HUMAN	P13232 homo sapien
2	895	97.1	177	2 Q8H2N1_SPRIM	Q8h2n1 papio cynoc
3	895	97.1	177	3 Q95U83_MACMU	Q95u83 macaca mula
4	679.5	73.7	176	1 IL7_SHEEP	Q28540 ovis aries
5	677.5	73.5	176	1 IL7_BOVIN	P26895 bos taurus
6	671.5	72.8	176	2 Q8HXR8_BOVIN	Q8hyr8 bos taurus
7	665	72.1	133	2 Q5FBY9_HUMAN	Q5fby9 homo sapien
8	663.5	72.0	176	2 Q9NZG6_PIG	Q9nzg6 sus scrofa
9	567	61.5	115	2 Q5FBX5_HUMAN	Q5fbx5 homo sapien
10	536.5	58.2	154	1 IL7_MOUSE	P10168 mus musculu
11	536.5	58.2	154	2 Q544C8_MOUSE	Q544c8 mus musculu
12	528.5	56.7	154	1 IL7_RAT	P56478 rattus norv
13	522.5	56.7	137	2 Q91Y32_RAT	Q91y32 rattus norv
14	445.5	48.3	137	2 Q8C9S3_MOUSE	Q8c9s3 mus musculu
15	308	33.4	64	2 Q5FBY5_HUMAN	Q5fby5 homo sapien
16	250	27.1	71	2 Q5FBY3_HUMAN	Q5fby3 homo sapien
17	164	17.8	37	2 Q5FBY6_HUMAN	Q5fby6 homo sapien
18	162	17.6	31	2 Q5FBY8_HUMAN	Q5fby8 homo sapien
19	94.5	10.2	2579	2 Q4UH03_THEAN	Q4uh03 thelleria a
20	93.5	10.1	671	2 Q39189_ARATH	Q39189 arabidopsis
21	89.5	9.7	671	2 Q94BX7_ARATH	Q94bx7 arabidopsis
22	89.5	9.7	671	2 Q91VB7_ARATH	Q91vb7 arabidopsis
23	87.5	9.5	1813	2 Q513P3_ENTHI	Q513p3 entamoeba h
24	87	9.4	578	2 Q42614_PLAAB	Q42614 plasmodium
25	87	9.4	1331	2 Q4YTD5_PLAAB	Q4ytd5 plasmodium
26	86.5	9.4	296	2 Q4HP36_CANUP	Q4hp36 campylobact
27	86.5	9.4	1241	2 Q9BP41_DROME	Q9bp41 drosophila
28	86.5	9.4	1241	2 Q9VWE7_DROME	Q9vwe7 drosophila
29	86	9.3	367	2 Q8PY40_METMA	Q8py40 metanostarc
30	85	9.2	901	2 Q6BY30_DEBHA	Q6by30 debaryomyce
31	85	9.2	1232	1 Y908_METJA	Q58318 methanococc

32	84.5	9.2	217	2 Q7XB9_BRANA	Q7xb9 brassica na
33	84.5	9.2	573	2 Q6BGL5_PASTE	Q6bgl5 pastereum
34	84.5	9.2	682	2 Q4YZJ1_PLAAB	Q4yzj1 plasmodium
35	84.5	9.2	838	1 CYAA_PSMU	Q05766 pasteurella
36	84.5	9.2	1111	2 Q9U0K5_PLAF7	Q9u0k5 plasmodium
37	84	9.1	812	2 Q8WY2_NEUCR	Q8wy2 neuropept
38	84	9.1	2661	2 Q81452_PLAF7	Q81452 plasmodium
39	83.5	9.1	1039	2 Q4XXB2_PLACH	Q4xxb2 plasmodium
40	83.5	9.1	1093	2 Q08204_YEAST	Q08204 saccharomyc
41	83.5	9.1	1123	2 Q9VKL5_DROME	Q9vkl5 drosophila
42	83.5	9.1	1349	2 Q62613_DROME	Q62613 drosophila
43	83.5	9.1	1365	2 Q62536_DROME	Q62536 drosophila
44	83.5	9.1	1365	2 Q62610_DROME	Q62610 drosophila
45	83.5	9.1	1365	2 Q9V463_DROME	Q9v463 drosophila

#### ALIGNMENTS

RESULT 1	ID	IL7_HUMAN	STANDARD	PRT	177 AA.
AC	P13232				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DE	10-MAY-2005 (Rel. 47, Last annotation update)				
DE	Interleukin-7 precursor (IL-7).				
GN	Name=IL7;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC	Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=89098903; PubMed=2643102;				
RA	Goodwin R.G., Lupton S., Schmieler A., Hjerrild K.J., Jerzy R.,				
RA	Cleaver W., Gillis S., Cosman D., Namen A.E.;				
RT	"Human interleukin 7: molecular cloning and growth factor activity on				
RT	human and murine B-lineage cells."				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:302-306(1989).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=90229755; PubMed=2329282;				
RA	Lupton S.D., Gimpel S., Jerzy R., Brunton L.L., Hjerrild K.A.,				
RA	Cosman D., Goodwin R.G.;				
RT	"Characterization of the human and murine IL-7 genes."				
RL	J. Immunol. 144:3592-3601(1990).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RC	TISSUE=pancreas;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;				
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Altschul S.F., Zeeberg B., Bueter K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Caavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smal M.A.;				
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[4]				

RP DISULFIDE BONDS, AND MASS SPECTROMETRY.  
 RA MEDLINE=98070497; PubMed=9407080; DOI=10.1074/jbc.272.52.32995;  
 RX Cosenza L., Sweeney E., Murphy J.R.;  
 RT "disulfide bond assignment in human interleukin-7 by matrix-assisted  
 laser desorption/ionization mass spectroscopy and site-directed  
 RT cyclase to serine mutational analysis.";  
 RL J. Biol. Chem. 272:32995-33000(1997).  
 RN [5]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=97015912; PubMed=8862549;  
 RA Kremer R.T., Dougherty S.W., Robinson A.J., Richard W.G.;  
 RT "Prediction of the three-dimensional structure of human interleukin-7  
 RT by homology modeling.";  
 RL Protein Eng. 9:493-498(1996).  
 RN [6]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=20306974; PubMed=10850801;  
 RA Cosenza L., Rosenbach A., White J.V., Murphy J.R., Smith T.F.;  
 RT "Comparative model building of interleukin-7 using interleukin-4 as a  
 RT template: a structural hypothesis that displays atypical surface  
 RT chemistry in helix D important for receptor activation.";  
 RL Protein Sci. 9:916-926(2000).  
 CC -1- FUNCTION: Hematopoietic growth factor capable of stimulating the  
 CC proliferation of lymphoid progenitors. It is important for  
 CC proliferation during certain stages of B-cell maturation.  
 CC -1- INTERACTION:  
 CC P13788:IL2RG; NDBxp=2; IntAct=EBI-80516, EBI-80475;  
 CC P16871:IL7R; NDBxp=3; IntAct=EBI-80516, EBI-80490;  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the IL-7/IL-9 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; J04156; AAA59156.1; -; mRNA.  
 DR EMBL; M29053; AAC63047.1; -; Genomic DNA.  
 DR EMBL; M29048; AAC63047.1; JOINED; Genomic DNA.  
 DR EMBL; M29049; AAC63047.1; JOINED; Genomic DNA.  
 DR EMBL; M29050; AAC63047.1; JOINED; Genomic DNA.  
 DR EMBL; M29051; AAC63047.1; JOINED; Genomic DNA.  
 DR EMBL; M29052; AAC63047.1; JOINED; Genomic DNA.  
 DR EMBL; BC047698; AAH47698.1; -; mRNA.  
 DR PIR; A43527; A32223.  
 DR PIR; B32223; B32223.  
 DR PIR; C32223; C32223.  
 DR PDB; 1IL7; Model; @=26-177.  
 DR IntAct; P13232; -;  
 DR Ensemble; ENSG00000104432; Homo sapiens.  
 DR HGNC; HGNC:6023; IL7.  
 DR MIM; 146660; -;  
 DR GO; GO:0005576; C:extracellular region; TAS.  
 DR GO; GO:0005139; F:interleukin-7 receptor binding; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006959; P:humoral immune response; TAS.  
 DR GO; GO:0009887; P:organogenesis; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR InterPro; IPR001181; Interleukin\_7.  
 DR InterPro; IPR000226; Interleukin\_9.  
 DR PANTHER; PTHR10526; Interleukin-7; 1.  
 DR Pfam; PF01415; IL7; 1.  
 DR PRINTS; PRSF001942; IL-7; 1.  
 DR PRODOM; PD013168; Interleukin-7; 1.  
 DR SMART; SM00127; IL7; 1.  
 DR PROSITE; PS00255; INTERLEUKIN\_7\_9; 1.  
 DR 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.  
 FT CHAIN 1 25 Interleukin-7.  
 FT CARBOHYD 95 95 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 116 116 N-linked (GlcNAc... ) (Potential).

FT CARBOHYD 141 141 N-linked (GlcNAc... ) (Potential).  
 FT DISULFID 27 166  
 FT DISULFID 59 154  
 FT DISULFID 72 117  
 FT HELIX 28 41  
 FT TURN 42 44  
 FT TURN 45 52  
 FT HELIX 71 89  
 FT HELIX 99 106  
 FT TURN 107 107  
 FT HELIX 108 119  
 FT TURN 120 120  
 FT HELIX 121 124  
 FT TURN 125 126  
 FT TURN 141 144  
 FT HELIX 147 172  
 SQ SEQUENCE 177 AA; 20187 MW; 8FC5243F9169617F CRC64;  
 Query Match 100.0%; Score 922; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 6,7e-76;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFHVSFRYIFGLPPLILVLPVASSDDIEKDKQYEVSLMVSIDQLDSMKRISNCL 60  
 DB 1 MFHVSFRYIFGLPPLILVLPVASSDDIEKDKQYEVSLMVSIDQLDSMKRISNCL 60  
 QY 61 NNEFNFFKRIHCDANKSGMFLFPAARKLRQFLKKNSTGDFLHLKYSGTTILNCTGQ 120  
 DB 61 NNEFNFFKRIHCDANKSGMFLFPAARKLRQFLKKNSTGDFLHLKYSGTTILNCTGQ 120  
 QY 121 VKGRPAALGSAOPTKSLSEKNSLKEQKNDLCFLKRLLOEIKTCWNKIMGTKEH 177  
 DB 121 VKGRPAALGSAOPTKSLSEKNSLKEQKNDLCFLKRLLOEIKTCWNKIMGTKEH 177  
 RESULT 2  
 Q8HZN1\_9PRIM PRELIMINARY; PRT; 177 AA.  
 AC Q8HZN1;  
 DT 01-MAR-2003 (TREMblrel. 23, Created)  
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Interleukin-7.  
 OS Papio cynocephalus x Papio anubis.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eumetazoa; Euarchontoglires; Primates; Catarrhini;  
 CC Cercopithecoidea; Cercopithecoidea; Papio.  
 OK NCBI\_TaxID=208510;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22617691; PubMed=12543864; DOI=10.1182/blood-2002-08-2671;  
 RA Storer J., Gilleady T. III, Lu H., Joseph A., Dawson M.A., Gough M.,  
 RA Morris J., Hackman R.C., Horn P.A., Sale G.E., Andrews R.G.,  
 RA Maloney D.G., Klem H.-P.;  
 RT "Interleukin-7 improves CD4 T-cell reconstitution after autologous  
 RT CD34 cell transplantation in monkeys.";  
 RL Blood 101:4209-4218(2003).  
 DR EMBL; AF541946; AAN17329.1; -; mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005139; F:interleukin-7 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR001181; Interleukin-7.  
 DR InterPro; IPR000226; Interleukin-7.  
 DR PANTHER; PTHR10526; Interleukin-7; 1.  
 DR Pfam; PF01415; IL7; 1.  
 DR PRINTS; PRSF001942; IL-7; 1.  
 DR PRODOM; PD013168; Interleukin-7; 1.  
 DR PROSITE; PS00255; INTERLEUKIN\_7\_9; 1.  
 SQ SEQUENCE 177 AA; 20230 MW; 11D6717EBB633424 CRC64;  
 Query Match 97.1%; Score 895; DB 2; Length 177;  
 Best Local Similarity 96.6%; Pred. No. 1.9e-73;  
 Matches 171; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

OY 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60
DB 1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMWSIDQLDSMKEIGSNCL 60
OY 61 NNEFNPFKXKHLCDANKEGMLFRAARKLQFLKMNSTGDPDLHLKVSSEGTILLNCTGQ 120
DB 61 NNEFNPFKXKHLCDANKEGMLFRAARKLQFLKMNSTGDPDLHLKVSSEGTILLNCTGK 120
OY 121 VGRKRPALGEPQPTKSLSEENKSLKEOKKLANDLCPFLKRLLOEIKTCWNKILMGTKKH 177
DB 121 VGRKRPALGEPQPTKSLSEENKSLKEOKKLANDSCFLKRLLOKIKTCWNKILMGTKKH 177

RESULT 3
O95J83_MACMU PRELIMINARY; PRT; 177 AA.
ID O95J83;
AC O95J83;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin 7.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopithecinae; Macaca.
OC NCBI_Taxid=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Gregoire A., Generario A.L., Morre M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401221; AK83922.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005139; P:interleukin-7 receptor binding; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR InterPro; IPR001181; Interleukin-7.
DR InterPro; IPR000226; Interleukin-7.
DR PANTHER; PTHR10526; Interleukin-7; 1.
DR Pfam; PF01415; IL7; 1.
DR PIRSF; PIRSF001942; IL-7; 1.
DR PRINTS; PRO0435; INTERLEUKIN7.
DR Prodom; PD013168; Interleukin-7; 1.
DR SMART; SM00127; IL7; 1.
SQ SEQUENCE 177 AA; 20230 MW; 11D6717EB863424 CRC64;

Query Match 97.1%; Score 895; DB 2; Length 177;
Best Local Similarity 96.6%; Pred. No. 1.9e-73;
Matches 171; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_Taxid=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph node;
RA MEDLINE=95197014; PubMed=7890175; DOI=10.1016/0378-1119(94)00857-O;
RA Barclam G.J., Andrews A.E., Nash A.D.;
RT Cloning and expression of a cDNA encoding ovine interleukin 7.;
RL Gene 154:265-269(1995).
CC -!- FUNCTION: Hematopoietic growth factor capable of stimulating the
CC proliferation of lymphoid progenitors. It is important for
CC proliferation during certain stages of B-cell maturation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-7/IL-9 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U10089; AAA78269.1; -; mRNA.
DR PIR; JC4035; JC4035.
DR HSSP; P13232; 1IL7.
DR InterPro; IPR001181; Interleukin-7.
DR InterPro; IPR000226; Interleukin-7.
DR PANTHER; PTHR10526; Interleukin-7; 1.
DR Pfam; PF01415; IL7; 1.
DR PIRSF; PIRSF001942; IL-7; 1.
DR PRINTS; PRO0435; INTERLEUKIN7.
DR Prodom; PD013168; Interleukin-7; 1.
DR SMART; SM00127; IL7; 1.
DR PROSITE; PS00255; INTERLEUKIN 7 9; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 25
FT CHAIN 26 176
FT CARBOHYD 94 94
FT CARBOHYD 115 115
FT CARBOHYD 140 140
FT DISULFID 27 165
FT DISULFID 58 153
FT DISULFID 71 116
SQ SEQUENCE 176 AA; 19983 MW; 87A448FD38142D17 CRC64;

Query Match 73.7%; Score 679.5; DB 1; Length 176;
Best Local Similarity 75.1%; Pred. No. 8.6e-54;
Matches 133; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

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Qy 1 MEHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQGYESVLWVSIDQLDSMKEIGSNCL 60
Db 1 MEHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQGYESVLWVSIDQLDSMKEIGSNCL 60
Qy 61 NNEFNFPRKHICDANKEGFLLPRAARKLRQFLKMNSTGDPDLHLKVSSEGTITLLNCTGQ 120
Db 61 NNEFNFPRKHICDANK----- 76
Qy 121 VGRKRPALGAEQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTYEH 177
Db 77 VGRKRPALGAEQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTYEH 133

RESULT 8
QSN2G6_PIG PRELIMINARY; PRT; 176 AA.
ID QSN2G6;
AC QSN2G6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Interleukin-7.
GN Name=IL-7; Synonyms=IL7;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxId=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=21240341; PubMed=11342229; DOI=10.1016/S0167-4781(00)00304-3;
RA Ueha S., Kikazawa H., Tomioka Y., Kawai T., Itoh T.;
RT "cDNA cloning and expression of swine IL-7 from neonatal intestinal
epithelium";
RL Biochim. Biophys. Acta 1517:468-471(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Uenishi H., Hiraiwa H., Sawazaki T., Kiuchi S., Yasue H.;
RT "Genomic organization and assignment of interleukin 7 gene (IL7) to
porcine chromosome 4q11-->q13 by FISH and by analysis of radiation
hybrid panels";
RL Cytogenet. Cell Genet. 0:0-0(2001).
DR EMBL; AB035380; BAA96385.1; -; mRNA.
DR EMBL; AB040441; BAB39170.1; -; mRNA.
DR EMBL; AB049332; BAB39172.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005139; F:interleukin-7 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001181; Interleukin-7.
DR InterPro; IPR000226; Interleukin-7_9.
DR PANTHER; PTHR10526; Interleukin-7; 1.
DR Pfam; PF01415; IL7; 1.
DR PRINTS; PIRSF001942; IL-7; 1.
DR PRINTS; PR00435; INTERLEUKIN7.
DR ProDom; PD013168; Interleukin-7; 1.
DR SMART; SM00127; IL7; 1.
SQ SEQUENCE 176 AA; 20161 MW; 9FB75E272BDCBBF CRC64;

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Query Match 72.0%; Score 663.5; DB 2; Length 176;
Best Local Similarity 72.9%; Pred. No. 2.5e-52;
Matches 129; Conservative 18; Mismatches 29; Indels 1; Gaps 1;
Qy 1 MEHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQGYESVLWVSIDQLDSMKEIGSNCL 60
Db 1 MEHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQGYESVLWVSIDQLDSMKEIGSNCL 59
Qy 61 NNEFNFPRKHICDANKEGFLLPRAARKLRQFLKMNSTGDPDLHLKVSSEGTITLLNCTGQ 120
Db 60 NNEFNFPRKHICDANKEGFLLPRAARKLRQFLKMNSTGDPDLHLKVSSEGTITLLNCTGQ 119
Qy 121 VGRKRPALGAEQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTYEH 177

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Db 120 VGRKRPALGAEQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTYEH 176

RESULT 9
QSFEX5_HUMAN PRELIMINARY; PRT; 115 AA.
ID QSFEX5;
AC QSFEX5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IL7 nrls variant 1.
GN Name=IL7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OC NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Samehima E., Tabata Y., Hayashi A., Iida K., Mitsuyama M., Kanai S.,
RA Furuya T., Saito T.;
RT "Interleukin7 mRNA, nrls splice variant1.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB102893; BAD89422.1; -; mRNA.
DR InterPro; IPR001181; Interleukin-7.
DR InterPro; IPR000226; Interleukin-7_9.
DR Pfam; PF01415; IL7; 1.
DR PRINTS; PR00435; INTERLEUKIN7.
DR ProDom; PD013168; Interleukin-7; 1.
DR SMART; SM00127; IL7; 1.
DR POSITE; PS00255; INTERLEUKIN 7_9; 1.
SQ SEQUENCE 115 AA; 13370 MW; B64APB2BBFE3E7E CRC64;

Query Match 61.5%; Score 567; DB 2; Length 115;
Best Local Similarity 65.0%; Pred. No. 9.5e-44;
Matches 115; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
Qy 1 MEHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQGYESVLWVSIDQLDSMKEIGSNCL 60
Db 1 MEHVSFRYIFGLPPLILVLLPVASSDCDIEGDKQGYESVLWVSIDQLDSMKEIGSNCL 60
Qy 61 NNEFNFPRKHICDANKEGFLLPRAARKLRQFLKMNSTGDPDLHLKVSSEGTITLLNCTGQ 120
Db 61 NNEFNFPRKHICDANK----- 76
Qy 121 VGRKRPALGAEQPTKSLSEENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTYEH 177
Db 77 -----EENKSLKEQKKLNDLCFLKRLLOEIKTCWNKILMGTYEH 115

RESULT 10
IL7_MOUSE STANDARD; PRT; 154 AA.
ID IL7_MOUSE;
AC P10168;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-7 precursor (IL-7).
GN Name=IL7; Synonyms=I1-7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=88232938; PubMed=3259677; DOI=10.1038/333571a0;
RA Namen A.E., Lupion S., Hjertild K., Wignall J., Mochizuki D.Y.,
RA Schriener A., Mosley B., March C.J., Urdal D., Gillis S., Cosman D.,
RA Goodwin R.G.;
RT "Stimulation of B-cell progenitors by cloned murine interleukin-7.";
RL Nature 333:571-573(1988).

```

[2]  
 RN NUCLEOTIDE SEQUENCE OF 1-119.  
 RP MEDLINE=90229755; PubMed=2329282;  
 RX Lupton S.D., Gimel S., Jerzy R., Brunton L.L., Hjertild K.A.,  
 RA Cosman D., Goodwin R.G.;  
 RT "Characterization of the human and murine IL-7 genes."  
 RL J. Immunol. 144:3592-3601 (1990).  
 CC -1- FUNCTION: Hematopoietic growth factor capable of stimulating the  
 CC proliferation of lymphoid progenitors. It is important for  
 CC proliferation during certain stages of B-cell maturation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PM: Three disulfide bonds are present (Probable).  
 CC -1- SIMILARITY: Belongs to the IL-7/IL-9 family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; X07962; CAA30779.1; -; mRNA.  
 DR EMBL; M29057; AAA39303.1; -; Genomic DNA.  
 DR EMBL; M29054; AAA39303.1; JOINED; Genomic DNA.  
 DR EMBL; M29055; AAA39303.1; JOINED; Genomic DNA.  
 DR EMBL; M29056; AAA39303.1; JOINED; Genomic DNA.  
 DR PIR; S03171; S03171.  
 DR HSSP; P13332; I117.  
 DR Ensemble; ENSMUSG0000040329; Mus musculus.  
 DR MGI; MGI:96561; I17.  
 DR GO; GO:0005125; F:cytokine activity; IDA.  
 DR GO; GO:0008083; F:growth factor activity; IDA.  
 DR GO; GO:0045453; P:bone resorption; IDA.  
 DR GO; GO:0043066; P:negative regulation of apoptosis; IDA.  
 DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.  
 DR GO; GO:0045582; P:positive regulation of T cell differentiation; IDA.  
 DR InterPro; IPR001181; Interleukin-7.  
 DR InterPro; IPR000226; Interleukin-7.  
 DR PANTHER; PTHR10526; Interleukin-7; 1.  
 DR Pfam; PF01415; IL7; 1.  
 DR PIRSF; PIRSF001942; IL-7; 1.  
 DR PRINTS; PR00435; INTERLEUKIN7.  
 DR ProDom; PD013168; Interleukin-7; 1.  
 DR SMART; SM00127; IL7; 1.  
 DR PROSITE; PS00255; INTERLEUKIN\_7\_9; 1.  
 DR KW Cytokine; Direct protein sequencing; Glycoprotein; Growth factor;  
 DR Signal.  
 FT CHAIN 1 25 Interleukin-7.  
 FT CARBOHYD 94 154 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 115 115 N-linked (GlcNAc... ) (Potential).  
 SQ SEQUENCE 154 AA; 17727 MW; CBAABVA1A7516A42 CRC64;  
 Query Match 58.2%; Score 536.5; DB 1; Length 154;  
 Best Local Similarity 61.5%; Pred. No. be-41; Indels 21; Gaps 3;  
 Matches 107; Conservative 21; Mismatches 25; Indels 21; Gaps 3;  
 QY 1 MFHVSFRITFGPLPILVILVLPASSDCDIEGDKGQYVSVLWVSIIDQLDLSMKEIGSNCL 60  
 DB 1 MFHVSFRITFGPLPILVILVLPASSDCDIEGDKGQYVSVLWVSIIDQLDLSMKEIGSNCL 59  
 QY 61 NNEFFEFKRIHICDANKGKMFLEFRARKIROPKRNKSTGDPDLHLIKVSEGTTLINCTGQ 120  
 DB 60 NNEFFEFKRIHICDANKGKMFLEFRARKIROPKRNKSTGDPDLHLIKVSEGTTLINCTGQ 118  
 QY 121 VKGRPALGEAQPTKSLSEKSKLKEOKKNDLCTGKRLDGEIKTCQNMKILMGT 174  
 DB 119 -----KEKNVKEQKK-NDACLKRLRLRIKTCQNMKILKGS 153  
 RESULT 11  
 ID 0544C8\_MOUSE PRELIMINARY; PRT; 154 AA.  
 AC 0544C8;

DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,  
 DE clone:4530098102 product:interleukin 7, full insert sequence.  
 GN Name=IL7,  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)00304-9;  
 RA Carinci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Watanabe T.,  
 RA Sakai K., Ohtsuki D., Fujuno M., Aono H., Baldarelli R., Barin G.,  
 RA Blake J., Bokfield D., Bojunga N., Carinci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiyama M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA MacLott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Natsushima T., Numa K., Okido T., Pavan W.J., Partea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sanderlin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of

[illegible]

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DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Interleukin-7 precursor (IL-7).
GN      Name=IL7;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxId=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=Fischer;
RA      Wiedgren B., Viase E., Sjogren H.O.;
RL      submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Hematopoietic growth factor capable of stimulating the
CC      proliferation of lymphoid progenitors. It is important for
CC      proliferation during certain stages of B-cell maturation.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- PM: Three disulfide bonds are present (Probable).
CC      -1- SIMILARITY: Belongs to the IL-7/IL-9 family.
CC      -----
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CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AF010464; AAB6350.1; -; mRNA.
DR      HSSP; P13232; IL7.
DR      Ensembl; ENSRNOG0000011973; Rattus norvegicus.
DR      RGD; 2904; IL7.
DR      InterPro; IPR001181; Interleukin-7.
DR      InterPro; IPR000226; Interleukin 7.
DR      PANTHER; PTHR10526; Interleukin-7; 1.
DR      Pfam; PF01415; IL7; 1.
DR      PIRSF; PIRSF001942; IL-7; 1.
DR      PRINTS; PR00435; INTERLEUKIN7.
DR      ProDom; PD013168; Interleukin-7; 1.
DR      SMART; SM00127; IL7; 1.
DR      PROSITE; PS00255; INTERLEUKIN 7 9; 1.
KW      Cytokine; Glycoprotein; Growth factor; Signal.
FT      SIGNAL          1           25
FT      CHAIN           26          154
FT      CABOHOYD        94           94
FT      CABOHOYD        115          115
SQ      SEQUENCE       154 AA; 17709 MW; 8D9E9E9FD0681741 CRC64;

Query Match          57.3%; Score 528.5; DB 1; Length 154;
Best Local Similarity 62.1%; Pred. No. 4; Je-40;
Matches 108; Conservative 19; Mismatches 26; Indels 21; Gaps 3;

Oy      1 MFHVSFYIIGLPLILVLTPVASSDDIDGKQKQYVESYLVMSIDPLDSMKRIGSNCL 60
Db      1 MFHVSFYIIGIPLILVLLPTVSSDCHIDKDGKAGSYLMISINQ-LDKMTGTSBDCP 59
Oy      61 NNEENFPRKRIIDANKEGMFLFPAARKLRQFLKKNSTGDFDLHLKVSSEGTLLNCTGQ 120
Db      60 NNEENFPRKRLCDPTKKAFLNPAARKLRQFLKKNSTSEENDHLRVSDFQTLVNTCTS- 118
Oy      121 VKGKKPALGDAOPTSKLEENKSLKEQKINDLCFLKRLLOEITKCNKILMGT 174
Db      119 -----KEEKTIKEQK-NDPCFLRLRLREIKTCWNKILKGS 153

RESULT 13
O91Y32_RAT PRELIMINARY; PRT; 154 AA.
AC O91Y32;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin-7.
SN Name=IL-7;
OS Rattus norvegicus (Rat).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISSUE=Spleen;  
 RA Bauer M., Friedl C., Wehr K., Schuppan D.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF367210; AAK53392.1; -, mRNA.  
 DR GO: GO:0005576; C:extracellular region; IEA.  
 DR GO: GO:0005139; F:interleukin-7 receptor binding; IEA.  
 DR GO: GO:0006955; P:immune response; IEA.  
 DR InterPro: IPR001181; Interleukin-7.  
 DR InterPro: IPR000226; Interleukin-7.  
 DR PANTHER: PTHR10526; Interleukin-7\_1.  
 DR Pfam: PF01415; IL7; 1. IL-7; 1.  
 DR PIRSF: PIRSF001942; IL-7; 1.  
 DR PRINTS: PR00435; INTERLEUKIN7.  
 DR ProDom: PD013168; Interleukin-7\_1.  
 DR PROSITE: PS00255; INTERLEUKIN 7\_9; 1.  
 DR SEQUENCE 154 AA; 17724 MW; 8D9E8358A0681741 CRC64;

Query Match 56.7%; Score 522.5; DB 2; Length 154;  
 Best Local Similarity 62.6%; Pred. No. 1,5e-39;  
 Matches 107; Conservative 18; Mismatches 25; Indels 21; Gaps 3;

Oy 1 MFHVSFRITFGIPILVILVLPVASSDCIIEGKQKQYSLVMSIDQLDSKKEIGSCL 60  
 Db 1 MFHVSFRITFGIPILVILVLPVSSDCHIKDKGAFPSVLMISINQ-LDKMTGDSDCP 59  
 Oy 61 NNEENFPRHICDANKEGMFLFRAARKLRDPLKKNSTDPDLHLIKVSEGTITLINTGQ 120  
 Db 60 NNEPFFPKKHCDDEKAEAFILRRARKLRQFLKKNISEEDHILRVSDGTQTVNCTS- 118  
 Oy 121 VKGRPALGEGQPTKSLSEKSKLSEOKKINDLCTLKLLDEIKTCNKKIL 171  
 Db 119 -----KEEKTIKEQKK-NDCPLKRLREIKTCNKKIL 150

RESULT 14  
 O8C9S3 MOUSE  
 ID O8C9S3; MOUSE PRELIMINARY; PRT; 137 AA.  
 AC O8C9S3;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched  
 DE library, clone:A630007F02 product:interleukin 7, full insert sequence.  
 DE (Fragment).  
 GN Name=IL7;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RT Mech. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gotojiori T., Bono H., Kanakawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzei J., Mommaerts P.,  
 RA Nordone P., Ring B., Ringuet M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA The RIKEN Consortium,  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).

RL [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki P.,  
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirokawa T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Karoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK041403; BAC30932.1; -, mRNA.  
 DR MGI: MGI:96561; IL7.  
 DR GO: GO:0005125; F:cytokine activity; IDA.  
 DR GO: GO:0008083; F:growth factor activity; IDA.  
 DR GO: GO:0045453; P:bone resorption; IDA.  
 DR GO: GO:0043066; P:negative regulation of apoptosis; IDA.  
 DR GO: GO:0030890; P:positive regulation of B-cell proliferation; IDA.  
 DR InterPro: IPR001181; Interleukin-7.  
 DR InterPro: IPR000226; Interleukin-7\_9.  
 DR PANTHER: PTHR10526; Interleukin-7\_1.  
 DR Pfam: PF01415; IL7; 1.  
 DR PIRSF: PIRSF001942; IL-7; 1.

DR PRINTS: PR00435; INTERLEUKIN7.  
DR PRODom: PD013168; Interleukin-7, 1.  
DR SMART; SM00127; IL7, 1.  
DR PROSITE; PS00255; INTERLEUKIN\_7\_9; 1.  
FT NON TER 1 1  
SQ SEQUENCE 137 AA; 15679 MW; 84CFEC

Query Match	48.3%	Score 445.5;	DB 2;	Length 137;
Best Local Similarity	58.0%;	Pred. No. 1.4e-32;		
Matches 91;	Conservative 20;	Mismatches 25;	Indels 21;	Gaps 3

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QY      18 VLLPVASDDIDGKQKQYSEVWYMSIQDILDSMKELISNCLNNEPNFPRKHICDANKE  77
      1 VLLPVATSSSECHIDKQKQKAYESVWYMSIDE-IDIMTGDSNCPNNEPNFPRKHVCDDTKE  59
QY      78 GMEFLFRAARKLROFLKNSTGDFDHLILKYSEGGTILLNCTGQVGRKPAALGEAQPTKS  137
Db      60 AAFANRAARKLKQFLKNNISSEEPNHHLLTVSGOTLVNCTS-----  101
QY      138 LEENKSLKEQKRLNDLCFLKRLILQEIKTQWNKILMGT  174
Db      102 -KEEKVYKEQK-NDACFLKRLILREIKTQWNKILKGS  136

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### RESULT 15

```
Q5FBY5 HUMAN
ID Q5FBY5_HUMAN PRELIMINARY; PRT; 64 AA
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DT 10-MAY-2005 (TREMBlere]. 30, Created)

DT	10-MAY-2005 (Tremblé)	30, Last sequence update)
DT	10-MAY-2005 (Tremblé)	30, Last annotation update)

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DE IL7 hrs variant 4.
GN Name=IL7;
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OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; C

0C Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae  
0C Homo.

OX	NCBI_1:ax1D=9606;
RN	[1]

RA Sameshima E., Tabata Y., Hayashi A., Iida K., Mitsuyama M., Kanai S.

RT "interleukin7 mRNA, nirs splice variant4.";

DR EMBL; AB102883; BAD89412.1; -; mRNA.  
 RL submitted (FEB-2003) to the EMBL/GenBank/DBJ databases

DR InterPro; IPR001181; Interleukin-7.  
DR InterPro; IPR000226; Interleukin\_7\_9.

DR ProDom; PD013168; Interleukin-7; 1.  
DR SMART; SM00127; IL7; 1.

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DR PROSITE; PS00255; INTERLEUKIN 7 9; 1.
SQ SEQUENCE 64 AA; 7687 MW; D03218F01F5AA3EA CRC64;
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Query Match	Score	DB 2	Length
33.4%	308	64	

Best Local Similarity 50.8%; Pred. NO. 26-20;  
Matches 64; Conservative 0; Mismatches 0; Indels 62; Gaps 1

52 MKEIGSNCLNNEFNFKRHC DANKEGNFLFRAARKLRQFLKMNSTGDFDLHLKIVSEGT 111

db 1 MKEIGSNCLNNEFNFKRHCDANK----- 25

112 TILNCTGVKGRKPAALGHAQPTKSLBENKSLKOKLNDICFLKRLLOEIKTCWKIL 171

db 26 -----EENKSLKEQKUNDLCPLKRLLEIKTCWNKIL 58

QY 172 MGTKEH 177

Db 59 MGTKEH 64

Search completed: December 29, 2005, 14:20:58  
Job time : 233 secs

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